Sheppard, Paula

From: Portner, Ginny
Sent: Tuesday, December 10, 2002 4:05 PM
To: Sheppard, Paula
Subject: 09/369,992

Importance: High

Paula, I left a voice mail but am also sending an email. You completed a sequence search of nucleotides 1147-1740 of SEQ ID No 1, but I also need a oligomer search of this specific region as well. Do I need to resubmit an additional search request? G

Ginny Portner
CM1, Art Unit 1645
Room 7e13
Mail box 7e12
(703) 308-7543

Interference search done

GS
12/11/02

Point of Contact
P. Sheppard
Telephone number: (703) 308-449[illegible]

12/13/02

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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 20:27:43 ; Search time 2430 Seconds
(without alignments)
3958.897 Million cell updates/sec

Title: US-09-369-992C-1_COPY_1147_1740
Perfect score: 594
Sequence: 1 gtatcgctttaataggcgaa.....ttacatctttcatgcaggtc 594

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description
c	1	93	15.7	636	17	AZ525208	AZ525208 241PbD09
	2	34	5.7	657	17	BH712144	BH712144 BOMDQ17TR
	3	34	5.7	706	17	BH515297	BH515297 BOHFD81TR
	4	34	5.7	733	17	BH691669	BH691669 BOMCZ07TF
	5	34	5.7	739	17	BH461405	BH461405 BOGTM02TF
	6	34	5.7	751	17	BH497288	BH497288 BOHIU64TF
	7	34	5.7	797	17	BH420610	BH420610 BOHGB03TR
	8	34	5.7	805	17	BH669801	BH669801 BOMOU92TR
c	9	33	5.6	121	17	BH593454	BH593454 BOHEI18TF
c	10	33	5.6	198	17	BH675598	BH675598 BOHYF27TF
	11	33	5.6	210	17	BH735917	BH735917 BOMBZ53TR
c	12	33	5.6	247	17	BH683107	BH683107 BOMLG07TR
	13	33	5.6	263	17	BH492660	BH492660 BOHJC63TF
	14	33	5.6	266	17	BH506879	BH506879 BOHKI70TR
	15	33	5.6	269	17	BH728745	BH728745 BOMMK86TR
	16	33	5.6	271	17	BH652699	BH652699 BOHYD05TF
c	17	33	5.6	275	17	BH603988	BH603988 BOGNL13TF
c	18	33	5.6	275	17	BH653527	BH653527 BOHXI13TR
c	19	33	5.6	284	17	BH739861	BH739861 gf20g12.b
	20	33	5.6	290	17	BH435779	BH435779 BOHID61TF
c	21	33	5.6	290	17	BH697699	BH697699 BOHYK49TF
c	22	33	5.6	292	17	BH684204	BH684204 BOMBQ32TF
c	23	33	5.6	309	17	BH015001	BH015001 TDGBT52TH
	24	33	5.6	313	17	BH567920	BH567920 BOHLK06TF
	25	33	5.6	319	17	BH599214	BH599214 BOHSD15TR
	26	33	5.6	333	13	BJ235085	BJ235085 BJ235085
c	27	33	5.6	336	17	BH015002	BH015002 TDGBT53TH
	28	33	5.6	336	17	BH655724	BH655724 BOHZU90TF
	29	33	5.6	337	17	BH430665	BH430665 BOHTO73TF
c	30	33	5.6	342	9	AA948766	AA948766 L0-286M13
	31	33	5.6	347	17	BH650187	BH650187 BOHUE15TR
c	32	33	5.6	351	17	BH463247	BH463247 BOGDJ95TF
c	33	33	5.6	366	17	BH593989	BH593989 BOHLQ17TR
	34	33	5.6	370	17	BH720360	BH720360 BOMLG55TF
	35	33	5.6	373	17	BH509392	BH509392 BOGGH73TF
c	36	33	5.6	377	13	BJ450787	BJ450787 BJ450787
c	37	33	5.6	381	10	AV556340	AV556340 AV556340
c	38	33	5.6	386	17	AQ843660	AQ843660 nbxb0024L
c	39	33	5.6	387	17	BH494088	BH494088 BOHTW03TR
	40	33	5.6	388	17	BH694769	BH694769 BOMIZ28TR
c	41	33	5.6	391	17	BH421905	BH421905 BOHND01TR
c	42	33	5.6	399	17	BH662429	BH662429 BOHZX27TF
	43	33	5.6	404	12	BF065393	BF065393 HV_CEb001
c	44	33	5.6	404	17	BH142535	BH142535 TDGDP86TH
	45	33	5.6	407	10	AV408731	AV408731 AV408731

ALIGNMENTS

RESULT 1
AZ525208/c
LOCUS AZ525208 636 bp DNA linear GSS 07-MAY-2001
DEFINITION 241PbD09 Pb MBN #21 Plasmodium berghei genomic 3', DNA sequence.
ACCESSION AZ525208
VERSION AZ525208.1 GI:13965828
KEYWORDS GSS.
SOURCE Plasmodium berghei.
ORGANISM Plasmodium berghei
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 636)
AUTHORS Carlton,J.M.-R. and Dame,J.B.
TITLE The Plasmodium vivax and P. berghei gene sequence tag projects
JOURNAL Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)
COMMENT Contact: Dame JB
Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
Tel: 352 392 4700
Fax: 352 392 9704
Email: damej@mail.vetmed.ufl.edu
Seq primer: M13(-20) forward
Class: shotgun.
FEATURES Location/Qualifiers
source 1. .636
/organism="Plasmodium berghei"
/strain="ANKA clone 15cy1 (clone of the ANKA 8417 clone)"
/db_xref="taxon:5821"
/clone_lib="Pb MBN #21"

/dev_stage="asexual blood forms"
/lab_host="Mus musculus"
/note="Vector: pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP; Site_1: EcoRV; Site_2: EcoRV; Genomic DNA was prepared from asynchronous blood stage forms of the cloned ANKA isolate of P. berghei grown in laboratory Swiss white mice. The DNA was purified from contaminating host DNA by Hoechst Dye 33258-CsCl ultracentrifugation and precipitated. Purified DNA was digested with mung bean nuclease in the presence of 36-38% formamide at 50 C, as described (Vernick, K.D., Imberski, R.B., and McCutchan, T.F. 1988. Nucleic Acids Research 16:6883-6896). The ends of the digestion fragments were polished using T4 DNA polymerase, and the fragments size selected in the range 500-2000 bp. These were ligated into the EcoRV-cleaved and dephosphorylated pBluescript SK(+) vector. Recombinant plasmids were used to transform E. coli XL10-Gold host cells. "
BASE COUNT 261 a 63 c 88 g 223 t 1 others
ORIGIN

Query Match 15.7%; Score 93; DB 17; Length 636;
Best Local Similarity 100.0%; Pred. No. 2.3e-30;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    502 TAATATAAGAAATCTGCATCTTCACAGATAATTTTATTTCATTAAGATTTTTTTTAAGAC 561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 TAATATAAGAAATCTGCATCTTCACAGATAATTTTATTTCATTAAGATTTTTTTTAAGAC 452

Qy    562 AGCATTTAAGTCGTTACATCTTTCATGCAGGTC 594
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Db    451 AGCATTTAAGTCGTTACATCTTTCATGCAGGTC 419
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RESULT 2
BH712144
LOCUS BH712144 657 bp DNA linear GSS 20-FEB-2002
DEFINITION BOMDQ17TR BO_2_3_KB Brassica oleracea genomic clone BOMDQ17, DNA sequence.
ACCESSION BH712144
VERSION BH712144.1 GI:18803004
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 657)
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOMDQ17TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES Location/Qualifiers
source 1. .657
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOMDQ17"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT 124 a 214 c 163 g 156 t
ORIGIN

Query Match 5.7%; Score 34; DB 17; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    116 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
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Db      5 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 38
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RESULT 3
BH515297
LOCUS BH515297 706 bp DNA linear GSS 13-DEC-2001
DEFINITION BOHFD81TR BOHF Brassica oleracea genomic clone BOHFD81, DNA sequence.
ACCESSION BH515297
VERSION BH515297.1 GI:17723387
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 706)
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOHFD81TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES Location/Qualifiers
source 1. .706
/organism="Brassica oleracea"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHFD81"
/clone_lib="BOHF"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT 131 a 228 c 177 g 170 t
ORIGIN

Query Match 5.7%; Score 34; DB 17; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    116 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
          ||||||||||||||||||||||||||||||||||
Db     29 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 62
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RESULT 4
BH691669
LOCUS BH691669 733 bp DNA linear GSS 19-FEB-2002
DEFINITION BOMCZ07TF BO_2_3_KB Brassica oleracea genomic clone BOMCZ07, DNA sequence.
ACCESSION BH691669
VERSION BH691669.1 GI:18762106
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 733)
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea

```
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOMCZ07TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .733
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOMCZ07"
                     /clone_lib="BO_2_3_KB"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      137 a    235 c    183 g    178 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0.00014;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    116 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
          ||||||||||||||||||||||||||||||||||
Db     32 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 65


RESULT 5
BH461405
LOCUS       BH461405                739 bp    DNA     linear   GSS 13-DEC-2001
DEFINITION  BOGTM02TF BOGT Brassica oleracea genomic clone BOGTM02, DNA
            sequence.
ACCESSION   BH461405
VERSION     BH461405.1  GI:17651151
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 739)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOGTM02TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .739
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOGTM02"
                     /clone_lib="BOGT"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      138 a    234 c    188 g    179 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0.00014;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    116 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
          ||||||||||||||||||||||||||||||||||
Db      8 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 41


RESULT 6
BH497288
LOCUS       BH497288                751 bp    DNA     linear   GSS 13-DEC-2001
DEFINITION  BOHIU64TF BOHI Brassica oleracea genomic clone BOHIU64, DNA
            sequence.
ACCESSION   BH497288
VERSION     BH497288.1  GI:17705392
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 751)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOHIU64TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .751
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOHIU64"
                     /clone_lib="BOHI"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      137 a    242 c    188 g    184 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0.00014;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    116 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
          ||||||||||||||||||||||||||||||||||
Db     32 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 65


RESULT 7
BH420610
LOCUS       BH420610                797 bp    DNA     linear   GSS 12-DEC-2001
DEFINITION  BOHGB03TR BOHG Brassica oleracea genomic clone BOHGB03, DNA
            sequence.
ACCESSION   BH420610
VERSION     BH420610.1  GI:17606338
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 797)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Chris Town
```

```
           TIGR
           9712 Medical Center Drive, Rockville, MD 20850, USA.
           Tel: 301-838-3523
           Fax: 301-838-0208
           Email: cdtown@tigr.org
           DNA is from a doubled haploid provided by Tom Osborn.
           Seq primer: TR
           Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .797
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOHGB03"
                     /clone_lib="BOHG"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      144 a    255 c    203 g    195 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0.00014;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    116 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
          ||||||||||||||||||||||||||||||||||
Db     29 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 62


RESULT 8
BH669801
LOCUS       BH669801                805 bp    DNA     linear   GSS 19-FEB-2002
DEFINITION  BOMOU92TR BO_2_3_KB Brassica oleracea genomic clone BOMOU92, DNA
            sequence.
ACCESSION   BH669801
VERSION     BH669801.1  GI:18732275
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 805)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .805
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOMOU92"
                     /clone_lib="BO_2_3_KB"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      145 a    258 c    205 g    197 t
ORIGIN

  Query Match             5.7%;  Score 34;  DB 17;  Length 805;
  Best Local Similarity   100.0%;  Pred. No. 0.00014;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    116 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
          ||||||||||||||||||||||||||||||||||
Db     35 TAGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 68


RESULT 9
BH593454/c
LOCUS       BH593454                121 bp    DNA     linear   GSS 15-DEC-2001
DEFINITION  BOHEI18TF BOHE Brassica oleracea genomic clone BOHEI18, DNA
            sequence.
ACCESSION   BH593454
VERSION     BH593454.1  GI:17845906
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 121)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOHEI18TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .121
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOHEI18"
                     /clone_lib="BOHE"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT       28 a     32 c     35 g     26 t
ORIGIN

  Query Match             5.6%;  Score 33;  DB 17;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 0.00075;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    117 AGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
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Db     53 AGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 21


RESULT 10
BH675598/c
LOCUS       BH675598                198 bp    DNA     linear   GSS 19-FEB-2002
DEFINITION  BOHYF27TF BO_2_3_KB Brassica oleracea genomic clone BOHYF27, DNA
            sequence.
ACCESSION   BH675598
VERSION     BH675598.1  GI:18745733
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 198)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
```

```
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES              Location/Qualifiers
     source           1. .198
                      /organism="Brassica oleracea"
                      /strain="TO1000DH3"
                      /db_xref="taxon:3712"
                      /clone="BOHYF27"
                      /clone_lib="BO_2_3_KB"
                      /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                      genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT       40 a     49 c     63 g     46 t
ORIGIN

  Query Match             5.6%;  Score 33;  DB 17;  Length 198;
  Best Local Similarity   100.0%;  Pred. No. 0.00062;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    117 AGCCTGTTATCCCTAGAGTAACTTTATCCGTT 149
          |||||||||||||||||||||||||||||||||
Db     69 AGCCTGTTATCCCTAGAGTAACTTTATCCGTT 37


RESULT 11
BH735917
LOCUS       BH735917                210 bp    DNA     linear   GSS 20-FEB-2002
DEFINITION  BOMBZ53TR BO_2_3_KB Brassica oleracea genomic clone BOMBZ53, DNA
            sequence.
ACCESSION   BH735917
VERSION     BH735917.1  GI:18841312
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 210)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOMBZ53TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES              Location/Qualifiers
     source           1. .210
                      /organism="Brassica oleracea"
                      /strain="TO1000DH3"
                      /db_xref="taxon:3712"
                      /clone="BOMBZ53"
                      /clone_lib="BO_2_3_KB"
                      /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                      genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT       48 a     68 c     50 g     44 t
ORIGIN

  Query Match             5.6%;  Score 33;  DB 17;  Length 210;
  Best Local Similarity   100.0%;  Pred. No. 0.00061;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    117 AGCCTGTTATCCCTAGAGTAACTTTATCCGTT 149
          |||||||||||||||||||||||||||||||||
Db    152 AGCCTGTTATCCCTAGAGTAACTTTATCCGTT 184


RESULT 12
BH683107/c
LOCUS       BH683107                247 bp    DNA     linear   GSS 19-FEB-2002
DEFINITION  BOMLG07TR BO_2_3_KB Brassica oleracea genomic clone BOMLG07, DNA
            sequence.
ACCESSION   BH683107
VERSION     BH683107.1  GI:18753550
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOMLG07TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES              Location/Qualifiers
     source           1. .247
                      /organism="Brassica oleracea"
                      /strain="TO1000DH3"
                      /db_xref="taxon:3712"
                      /clone="BOMLG07"
                      /clone_lib="BO_2_3_KB"
                      /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                      genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT       61 a     64 c     80 g     42 t
ORIGIN

  Query Match             5.6%;  Score 33;  DB 17;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 0.00057;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    117 AGCCTGTTATCCCTAGAGTAACTTTATCCGTT 149
          |||||||||||||||||||||||||||||||||
Db    197 AGCCTGTTATCCCTAGAGTAACTTTATCCGTT 165


RESULT 13
BH492660
LOCUS       BH492660                263 bp    DNA     linear   GSS 13-DEC-2001
DEFINITION  BOHJC63TF BOHJ Brassica oleracea genomic clone BOHJC63, DNA
            sequence.
ACCESSION   BH492660
VERSION     BH492660.1  GI:17700764
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 263)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOHJC63TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
```

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           Seq primer: TF
           Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .263
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOHJC63"
                     /clone_lib="BOHJ"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT       59 a     84 c     63 g     57 t
ORIGIN

  Query Match             5.6%;  Score 33;  DB 17;  Length 263;
  Best Local Similarity   100.0%;  Pred. No. 0.00056;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     117 AGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
           |||||||||||||||||||||||||||||||||
Db     177 AGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 209


RESULT 14
BH506879
LOCUS       BH506879                 266 bp    DNA     linear   GSS 13-DEC-2001
DEFINITION  BOHKI70TR BOHK Brassica oleracea genomic clone BOHKI70, DNA
            sequence.
ACCESSION   BH506879
VERSION     BH506879.1  GI:17714976
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 266)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOHKI70TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .266
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOHKI70"
                     /clone_lib="BOHK"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT       53 a     84 c     68 g     61 t
ORIGIN

  Query Match             5.6%;  Score 33;  DB 17;  Length 266;
  Best Local Similarity   100.0%;  Pred. No. 0.00056;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     117 AGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
           |||||||||||||||||||||||||||||||||
Db     117 AGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149


RESULT 15
BH728745
LOCUS       BH728745                 269 bp    DNA     linear   GSS 20-FEB-2002
DEFINITION  BOMMK86TR BO_2_3_KB Brassica oleracea genomic clone BOMMK86, DNA
            sequence.
ACCESSION   BH728745
VERSION     BH728745.1  GI:18834140
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 269)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOMMK86TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .269
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOMMK86"
                     /clone_lib="BO_2_3_KB"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT       61 a     87 c     62 g     59 t
ORIGIN

  Query Match             5.6%;  Score 33;  DB 17;  Length 269;
  Best Local Similarity   100.0%;  Pred. No. 0.00056;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     117 AGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
           |||||||||||||||||||||||||||||||||
Db     218 AGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 250


Search completed: December 11, 2002, 22:11:03
Job time : 2437 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 20:30:23 ; Search time 69 Seconds
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2640.087 Million cell updates/sec

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Perfect score: 594
Sequence: 1 gtatcgctttaataggcgaa.....ttacatctttcatgcaggtc 594

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	27	4.5	2904	4	US-09-465-355-3	Sequence 3, Appli
c	2	25	4.2	1869	2	US-08-371-377-21	Sequence 21, Appl
c	3	24	4.0	294	4	US-09-134-001C-235	Sequence 235, App
c	4	24	4.0	294	4	US-09-134-001C-889	Sequence 889, App
c	5	24	4.0	294	4	US-09-134-001C-1038	Sequence 1038, Ap
c	6	24	4.0	294	4	US-09-134-001C-1355	Sequence 1355, Ap
c	7	24	4.0	294	4	US-09-134-001C-2007	Sequence 2007, Ap
c	8	24	4.0	321	4	US-09-134-001C-475	Sequence 475, App
c	9	24	4.0	8411	4	US-08-961-527-16	Sequence 16, Appl
	10	23	3.9	3268	4	US-09-221-017B-981	Sequence 981, App
c	11	23	3.9	3901	4	US-09-221-017B-1043	Sequence 1043, Ap
c	12	23	3.9	4411529	4	US-09-103-840A-1	Sequence 1, Appli
c	13	22	3.7	2542	4	US-09-187-946-3	Sequence 3, Appli
c	14	20	3.4	1146	4	US-09-149-476-247	Sequence 247, App
c	15	20	3.4	1186	4	US-09-149-476-89	Sequence 89, Appl
	16	20	3.4	1530	5	PCT-US96-05320A-899	Sequence 899, App
c	17	19	3.2	369	1	US-08-530-010-21	Sequence 21, Appl
c	18	19	3.2	369	1	US-08-484-101B-21	Sequence 21, Appl
c	19	19	3.2	369	4	US-08-714-524D-21	Sequence 21, Appl
	20	19	3.2	740	4	US-08-998-416-771	Sequence 771, App
c	21	19	3.2	2787	1	US-08-530-010-2	Sequence 2, Appli
c	22	19	3.2	2787	1	US-08-530-010-4	Sequence 4, Appli
c	23	19	3.2	2787	1	US-08-530-010-6	Sequence 6, Appli
c	24	19	3.2	2787	1	US-08-530-010-8	Sequence 8, Appli
c	25	19	3.2	2787	1	US-08-530-010-10	Sequence 10, Appl
c	26	19	3.2	2787	1	US-08-484-101B-2	Sequence 2, Appli
c	27	19	3.2	2787	1	US-08-484-101B-4	Sequence 4, Appli
c	28	19	3.2	2787	1	US-08-484-101B-6	Sequence 6, Appli
c	29	19	3.2	2787	1	US-08-484-101B-8	Sequence 8, Appli
c	30	19	3.2	2787	1	US-08-484-101B-10	Sequence 10, Appl
c	31	19	3.2	2787	4	US-08-714-524D-2	Sequence 2, Appli
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c	35	19	3.2	2787	4	US-08-714-524D-10	Sequence 10, Appl
c	36	19	3.2	3552	4	US-09-157-210-3	Sequence 3, Appli
	37	19	3.2	3567	2	US-09-166-203-1	Sequence 1, Appli
	38	19	3.2	3567	4	US-09-377-309-1	Sequence 1, Appli
c	39	19	3.2	3879	1	US-08-530-010-1	Sequence 1, Appli
c	40	19	3.2	3879	1	US-08-484-101B-1	Sequence 1, Appli
c	41	19	3.2	3879	4	US-08-714-524D-1	Sequence 1, Appli
c	42	18	3.0	207	4	US-09-134-001C-239	Sequence 239, App
c	43	18	3.0	207	4	US-09-134-001C-498	Sequence 498, App
c	44	18	3.0	207	4	US-09-134-001C-893	Sequence 893, App
c	45	18	3.0	207	4	US-09-134-001C-1061	Sequence 1061, Ap

ALIGNMENTS

RESULT 1
US-09-465-355-3/c
; Sequence 3, Application US/09465355
; Patent No. 6316194
; GENERAL INFORMATION:
; APPLICANT: Karn, Jonathan
; APPLICANT: Knowles, David
; APPLICANT: Murchie, Alastair
; APPLICANT: Lentzen, Georg
; TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Antimicrobials
; FILE REFERENCE: 22620/1150 (Formerly 3950/85276)
; CURRENT APPLICATION NUMBER: US/09/465,355
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/325,601
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: GB 9812196.5
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: GB 9904790.4
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/122,439
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: US 60/088,241
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2904
; TYPE: RNA
; ORGANISM: Escherichia coli
US-09-465-355-3

Query Match 4.5%; Score 27; DB 4; Length 2904;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
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Db   2267 TAGGAGGAGACCGCCCCAGTCAAACTA 2241
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RESULT 2
US-08-371-377-21/c
; Sequence 21, Application US/08371377
; Patent No. 5851764
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Shen, Ruoqian
; TITLE OF INVENTION: DEVELOPMENT OF DNA PROBES AND
; TITLE OF INVENTION: IMMUNOLOGICAL REAGENTS SPECIFIC FOR CELL SURFACE-EXPRESSED
; TITLE OF INVENTION: MOLECULES AND TRANSFORMATION-ASSOCIATED GENES

```
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/371,377
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0575/37590-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1869 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-371-377-21

  Query Match             4.2%;  Score 25;  DB 2;  Length 1869;
  Best Local Similarity   100.0%;  Pred. No. 0.021;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      63 AGCCGACATCGAGGTGCCAAACCTT 87
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Db    1759 AGCCGACATCGAGGTGCCAAACCTT 1735


RESULT 3
US-09-134-001C-235/c
; Sequence 235, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 235
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-235

  Query Match             4.0%;  Score 24;  DB 4;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 0.073;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      63 AGCCGACATCGAGGTGCCAAACCT 86
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Db    175 AGCCGACATCGAGGTGCCAAACCT 152


RESULT 4
US-09-134-001C-889/c
; Sequence 889, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 889
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-889

  Query Match             4.0%;  Score 24;  DB 4;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 0.073;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      63 AGCCGACATCGAGGTGCCAAACCT 86
           ||||||||||||||||||||||||
Db    175 AGCCGACATCGAGGTGCCAAACCT 152


RESULT 5
US-09-134-001C-1038/c
; Sequence 1038, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1038
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1038

  Query Match             4.0%;  Score 24;  DB 4;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 0.073;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      63 AGCCGACATCGAGGTGCCAAACCT 86
           ||||||||||||||||||||||||
Db    175 AGCCGACATCGAGGTGCCAAACCT 152


RESULT 6
US-09-134-001C-1355/c
; Sequence 1355, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
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;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1355
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1355

  Query Match             4.0%;  Score 24;  DB 4;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 0.073;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      63 AGCCGACATCGAGGTGCCAAACCT 86
           ||||||||||||||||||||||||
Db     175 AGCCGACATCGAGGTGCCAAACCT 152


RESULT 7
US-09-134-001C-2007/c
; Sequence 2007, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2007
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2007

  Query Match             4.0%;  Score 24;  DB 4;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 0.073;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      63 AGCCGACATCGAGGTGCCAAACCT 86
           ||||||||||||||||||||||||
Db     175 AGCCGACATCGAGGTGCCAAACCT 152


RESULT 8
US-09-134-001C-475/c
; Sequence 475, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 475
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-475

  Query Match             4.0%;  Score 24;  DB 4;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 0.072;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      63 AGCCGACATCGAGGTGCCAAACCT 86
           ||||||||||||||||||||||||
Db     175 AGCCGACATCGAGGTGCCAAACCT 152


RESULT 9
US-08-961-527-16/c
; Sequence 16, Application US/08961527
; Patent No. 6420135
;  GENERAL INFORMATION:
;    APPLICANT:  Charles Kunsch
;    TITLE OF INVENTION:  Streptococcus pneumoniae Polynucleotides and Sequences
;    NUMBER OF SEQUENCES:  391
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/961,527
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brookes, A. Anders
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB340P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8411 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-961-527-16

  Query Match             4.0%;  Score 24;  DB 4;  Length 8411;
  Best Local Similarity   100.0%;  Pred. No. 0.049;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      63 AGCCGACATCGAGGTGCCAAACCT 86
           ||||||||||||||||||||||||
Db      32 AGCCGACATCGAGGTGCCAAACCT 9


RESULT 10
US-09-221-017B-981
; Sequence 981, Application US/09221017B
; Patent No. 6444799
;  GENERAL INFORMATION:
;    APPLICANT:  Ross, Bruce C.
;    TITLE OF INVENTION:  P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
;    NUMBER OF SEQUENCES:  1120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
```

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;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/221,017B
;      FILING DATE:  23-DEC-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP1182
;      FILING DATE:  31-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP1546
;      FILING DATE:  30-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP2911
;      FILING DATE:  09-APR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/AU98/01023
;      FILING DATE:  10-DEC-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monroy, Gladys H
;      REGISTRATION NUMBER:  32,430
;      REFERENCE/DOCKET NUMBER:  27340-20021.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  981:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3268 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  UNKNOWN
;    ORIGINAL SOURCE:
;      ORGANISM:  PORYPHYROMONAS GINGIVALIS
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1...3268
US-09-221-017B-981

  Query Match             3.9%;  Score 23;  DB 4;  Length 3268;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      63 AGCCGACATCGAGGTGCCAAACC 85
           |||||||||||||||||||||||
Db    2896 AGCCGACATCGAGGTGCCAAACC 2918


RESULT 11
US-09-221-017B-1043/c
; Sequence 1043, Application US/09221017B
; Patent No. 6444799
;  GENERAL INFORMATION:
;    APPLICANT:  Ross, Bruce C.
;    TITLE OF INVENTION:  P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
;    NUMBER OF SEQUENCES:  1120
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/221,017B
;      FILING DATE:  23-DEC-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP1182
;      FILING DATE:  31-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP1546
;      FILING DATE:  30-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PP2911
;      FILING DATE:  09-APR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/AU98/01023
;      FILING DATE:  10-DEC-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Monroy, Gladys H
;      REGISTRATION NUMBER:  32,430
;      REFERENCE/DOCKET NUMBER:  27340-20021.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-813-5600
;      TELEFAX:  650-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  1043:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3901 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  UNKNOWN
;    ORIGINAL SOURCE:
;      ORGANISM:  PORYPHYROMONAS GINGIVALIS
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1...3901
US-09-221-017B-1043

  Query Match             3.9%;  Score 23;  DB 4;  Length 3901;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      63 AGCCGACATCGAGGTGCCAAACC 85
           |||||||||||||||||||||||
Db    1902 AGCCGACATCGAGGTGCCAAACC 1880


RESULT 12
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
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;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             3.9%;  Score 23;  DB 4;  Length 4411529;
  Best Local Similarity   100.0%;  Pred. No. 0.065;
  Matches   23;  Conservative   0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      63 AGCCGACATCGAGGTGCCAAACC 85
           |||||||||||||||||||||||
Db 1476404 AGCCGACATCGAGGTGCCAAACC 1476382


RESULT 13
US-09-187-946-3/c
; Sequence 3, Application US/09187946
; Patent No. 6255467
; GENERAL INFORMATION:
;  APPLICANT: Lindner, Luther E.
;  APPLICANT: Macphee, Kathleen
;  TITLE OF INVENTION: Human Blood Bacterium
;  FILE REFERENCE: D6026
;  CURRENT APPLICATION NUMBER: US/09/187,946
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: US 60/064,472
;  EARLIER FILING DATE: 1997-11-06
;  NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 3
;   LENGTH: 2542
;   TYPE: DNA
;   ORGANISM: unknown
;   FEATURE:
;   OTHER INFORMATION: Rb 23S rRNA sequence of a new human blood bacterium
US-09-187-946-3

  Query Match             3.7%;  Score 22;  DB 4;  Length 2542;
  Best Local Similarity   100.0%;  Pred. No. 0.43;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      63 AGCCGACATCGAGGTGCCAAAC 84
           ||||||||||||||||||||||
Db   2311 AGCCGACATCGAGGTGCCAAAC 2290


RESULT 14
US-09-149-476-247/c
; Sequence 247, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,333
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/038,621
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,626
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,334
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,336
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,163
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/047,600
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,615
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,597
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,502
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,633
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,583
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,617
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,618
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,503
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,592
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,581
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,584
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,500
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,587
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,492
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,598
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,613
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,582
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,596
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,612
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,632
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/047,601
;  EARLIER FILING DATE: 1997-05-23
;  EARLIER APPLICATION NUMBER: 60/043,580
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,568
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,314
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,569
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,311
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,671
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,674
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,669
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,312
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,313
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,672
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/043,315
;  EARLIER FILING DATE: 1997-04-11
;  EARLIER APPLICATION NUMBER: 60/048,974
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/056,886
;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/056,877
;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/056,889
;  EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-09-05
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; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 3.4%; Score 20; DB 4; Length 1146;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    234 TATATATTTATCTTTATATA 253
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Db    481 TATATATTTATCTTTATATA 462
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RESULT 15
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; Sequence 89, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
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Query Match 3.4%; Score 20; DB 4; Length 1186;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 2898 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 19:01:38 ; Search time 304 Seconds
(without alignments)
4400.286 Million cell updates/sec

Title: US-09-369-992C-1_COPY_1147_1740
Perfect score: 594
Sequence: 1 gtatcgctttaataggcgaa.....ttacatctttcatgcaggtc 594

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1		594	100.0	5849	19	AAV33135	Plasmodium berghei
2		33	5.6	134525	11	AAQ04525	Total base sequenc
c 3		33	5.6	134525	11	AAQ04525	Total base sequenc
c 4		27	4.5	638	22	AAC89401	E.coli 23S rRNA DN
5		27	4.5	813	23	AAS82419	DNA encoding novel
c 6		27	4.5	1258	24	AAK99200	1258nt of E-site R
c 7		27	4.5	1446	23	AAS87232	DNA encoding novel
c 8		27	4.5	2115	23	AAS77887	DNA encoding novel
9		27	4.5	2904	21	AAA66047	E. coli proliferat
10		27	4.5	2904	21	AAA66052	E. coli proliferat
c 11		27	4.5	2904	22	AAH75411	E. coli 23S rRNA.
c 12		27	4.5	2904	22	AAF23016	E. coli 23S rRNA s
c 13		27	4.5	2904	22	AAC89403	Sequences from 23S
c 14		27	4.5	2907	19	AAV38096	Enterohaemorrhagic
c 15		27	4.5	2907	19	AAV38107	Enterohaemorrhagic
16		27	4.5	2910	23	AAS82418	DNA encoding novel
17		27	4.5	2910	23	AAS93250	DNA encoding novel
c 18		27	4.5	2958	23	AAS86736	DNA encoding novel
c 19		27	4.5	3067	23	AAS89786	DNA encoding novel
c 20		27	4.5	3118	22	AAH49806	Escherichia coli t
21		27	4.5	3687	23	AAS90090	DNA encoding novel
22		27	4.5	3756	23	AAS93772	DNA encoding novel
c 23		27	4.5	5013	20	AAX24985	E. coli MG1655 rrn
c 24		27	4.5	5014	20	AAX24987	E. coli MG1655 rrn
25		27	4.5	5090	20	AAX24988	E. coli MG1655 rrn
c 26		27	4.5	5097	20	AAX24983	E. coli MG1655 rrn
c 27		27	4.5	5098	20	AAX24984	E. coli MG1655 rrn
c 28		27	4.5	5105	20	AAX24989	E. coli MG1655 rrn
29		27	4.5	5162	23	AAS88965	DNA encoding novel
30		27	4.5	5341	20	AAX24986	E. coli MG1655 rrn
c 31		27	4.5	105184	24	ABK24122	Bacterial artifici
32		27	4.5	269223	22	AAF28554	Genomic fragment #
33		25	4.2	444	13	AAQ31812	Astrovirus serotyp
c 34		25	4.2	1869	17	AAT37413	Prostate tumour in
c 35		25	4.2	2940	24	ABL54765	Lactobacillus plan
c 36		25	4.2	5273	20	AAX24982	Haemophilus influe
c 37		25	4.2	5519	20	AAX24981	Haemophilus influe
38		25	4.2	640681	24	ABA92787	Buchnera sp. genom
39		25	4.2	1830121	17	AAT42063	Haemophilus influe
40		24	4.0	24	19	AAV33153	Plasmodium berghei
c 41		24	4.0	55	18	AAV79333	Staphylococcus aur
42		24	4.0	97	23	AAS50394	Staphylococcus aur
43		24	4.0	120	18	AAV79107	Staphylococcus aur
44		24	4.0	135	18	AAV79076	Staphylococcus aur
45		24	4.0	136	18	AAV79080	Staphylococcus aur

ALIGNMENTS

RESULT 1
AAV33135
ID AAV33135 standard; DNA; 5849 BP.
XX
AC AAV33135;
XX
DT 07-DEC-1998 (first entry)
XX
DE Plasmodium berghei plastid PS1-PL470 gene.
XX
KW Malaria; infection; therapy; diagnosis; vaccine; plastid;
KW PS1-PL470 gene; ds.
XX
OS Plasmodium berghei ANKA strain.
XX
PN WO9835057-A1.
XX
PD 13-AUG-1998.
XX
PF 05-FEB-1998; 98WO-IB00212.
XX
PR 26-SEP-1997; 97AU-0009481.
PR 06-FEB-1997; 97AU-0004953.
PR 21-APR-1997; 97AU-0006329.
XX
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
PA (UYSI-) UNIV SINGAPORE NAT.
XX
PI Kara AKU, Nelson JS, Tan TMC, Tham JM, Ting RCY;
XX
DR WPI; 1998-447251/38.
XX

```
PT   Detecting Plasmodium infection from hybridisation with
PT   extrachromosomal element - providing genus or species specific
PT   diagnosis with few false negatives, in humans or animals
XX
PS   Claim 15; Page 54-59; 120pp; English.
XX
CC   This is the nucleotide sequence of one strand of the PS1-PL470
CC   gene of the 30.7 kb extrachromosomal plastid of Plasmodium berghei.
CC   This plastid encodes organelle-like rRNAs, tRNAs, ribosomal
CC   proteins and RNA polymerase subunits, amongst others.  Plasmodium is
CC   detected in a human or animal sample by treating it, or derived
CC   nucleic acid, with a Plasmodium extrachromosomal genetic element or
CC   derived nucleic acid (A) and detecting any hybridisation.  (A) can
CC   include the PS1-PL470, PLH-PPH, PRB or PWQ gene, the mitochondrial
CC   coxI gene, and nucleic acids derived from them.  Also new are
CC   (A)-specific probes and primers (see AAV33139-56).  The method is
CC   used to diagnose Plasmodium infection.  Also (not claimed) the
CC   polypeptides encoded by (A) are useful as targets for drug
CC   development and for development of anti-malaria vaccines.  The high
CC   degree of similarity between (A) from different species allows
CC   development of genus- or species-specific assays that result in
CC   fewer false negatives than known methods (typically 1% against 3%).
XX
SQ   Sequence 5849 BP; 2296 A; 673 C; 557 G; 2323 T; 0 other;

  Query Match             100.0%;  Score 594;  DB 19;  Length 5849;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-261;
  Matches  594;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    1147 GTATCGCTTTAATAGGCGAACAGACTTACCCTTAAAACATACTACTGCCTTAGGATGCGA 1206

Qy      61 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAAGATTAGCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1207 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAAGATTAGCC 1266

Qy     121 TGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTATTAAATAATTATCG 180
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Db    1267 TGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTATTAAATAATTATCG 1326

Qy     181 GATCATTAAGACCGACATTAATCTCTGTTTAATTTGTAAATTTTACAGTTAATTATATAT 240
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Qy     241 TTATCTTTATATAATAAATATAACATTGTACACCTCCGTTTTTATATAGGAGGAGACCGC 300
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Db    1387 TTATCTTTATATAATAAATATAACATTGTACACCTCCGTTTTTATATAGGAGGAGACCGC 1446

Qy     301 CCCAGTCAAACTATCTTATAAATATTGTTAAAAATTTTGTTATAAAAATTTTATAAGAAT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1447 CCCAGTCAAACTATCTTATAAATATTGTTAAAAATTTTGTTATAAAAATTTTATAAGAAT 1506

Qy     361 TTATATATATATAAAATGGTATTTCATTAACAATTACATTATTTCCAAAAAAATAATATT 420
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Qy     421 ACTACTTCCCATTTATTCTATGTTATATATATATATTTTCAATATCTATTAATAGTAAAG 480
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Qy     481 CTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGCATCTTCACAGATAATTTTATTT 540
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Qy     541 CATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAGGTC 594
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RESULT 2
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ID   AAQ04525 standard; DNA; 134525 BP.
XX
AC   AAQ04525;
XX
DT   01-OCT-1990  (first entry)
XX
DE   Total base sequence of rice plant chloroplast DNA.
XX
KW   Chloroplast; true grass; rice plant; ss.
XX
OS   Oryza sativa.
XX
PN   JP02100682-A.
XX
PD   12-APR-1990.
XX
PF   07-OCT-1988;   88JP-0251967.
XX
PR   07-OCT-1988;   88JP-0251967.
XX
PA   (MITK ) MITSUI TOATSU CHEM INC.
XX
DR   WPI; 1990-159709/21.
XX
PT   Chloroplast DNA of true grasses - used to produce various
PT   DNA base sequences by decomposition of rice plant DNA.
XX
PS   Claim 1; Fig 1; 20pp; Japanese.
XX
CC   The sequence is that of the whole of rice chloroplast DNA.
XX
SQ   Sequence 134525 BP; 41249 A; 26129 C; 26331 G; 40816 T; 0 other;

  Query Match              5.6%;  Score 33;  DB 11;  Length 134525;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-05;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     117 AGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
           |||||||||||||||||||||||||||||||||
Db 117355 AGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 117387


RESULT 3
AAQ04525/c
ID   AAQ04525 standard; DNA; 134525 BP.
XX
AC   AAQ04525;
XX
DT   01-OCT-1990  (first entry)
XX
DE   Total base sequence of rice plant chloroplast DNA.
XX
KW   Chloroplast; true grass; rice plant; ss.
XX
OS   Oryza sativa.
XX
PN   JP02100682-A.
XX
PD   12-APR-1990.
XX
PF   07-OCT-1988;   88JP-0251967.
XX
PR   07-OCT-1988;   88JP-0251967.
XX
PA   (MITK ) MITSUI TOATSU CHEM INC.
XX
DR   WPI; 1990-159709/21.
XX
PT   Chloroplast DNA of true grasses - used to produce various
PT   DNA base sequences by decomposition of rice plant DNA.
XX
PS   Claim 1; Fig 1; 20pp; Japanese.
XX
CC   The sequence is that of the whole of rice chloroplast DNA.
```

```
XX
SQ   Sequence 134525 BP; 41249 A; 26129 C; 26331 G; 40816 T; 0 other;

  Query Match             5.6%;  Score 33;  DB 11;  Length 134525;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-05;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    117 AGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 149
          |||||||||||||||||||||||||||||||||
Db  97763 AGCCTGTTATCCCTAGAGTAACTTTTATCCGTT 97731


RESULT 4
AAC89401/c
ID   AAC89401 standard; DNA; 638 BP.
XX
AC   AAC89401;
XX
DT   08-MAR-2001  (first entry)
XX
DE   E.coli 23S rRNA DNA.
XX
KW   23S rRNA; ribosomal polynucleotide; infection; otitis media;
KW   conjunctivitis; pneumonia; bacteremia; meningitis; sinusitis;
KW   pleural empyema; endocarditis; ds.
XX
OS   Escherichia coli.
XX
PN   WO200071560-A1.
XX
PD   30-NOV-2000.
XX
PF   04-MAY-2000; 2000WO-US12133.
XX
PR   20-MAY-1999;   99US-0134973.
PR   07-JUN-1999;   99US-0137837.
PR   14-JUN-1999;   99US-0139095.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Hegg LA,  Sterner TA;
XX
DR   WPI; 2001-102280/11.
XX
PT   Novel bacterial ribosomal polynucleotides useful for identifying
PT   agonists and antagonists for treating otitis media, conjunctivitis,
PT   pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and
PT   endocarditis  -
XX
PS   Claim 1; Page 16; 67pp; English.
XX
CC   The present invention relates to Escherichia coli 23S rRNA.
CC   Derivatives from this protein may be useful for treating an
CC   individual having a need to inhibit a ribosomal polynucleotide.
CC   Agonists and antagonists identified are useful for treating an
CC   individual infected by Staphylococcus aureus or Streptococcus
CC   pneumoniae. The DNA sequence may also be used in the
CC   discovery and screening of antibacterial drugs, and its respective
CC   mRNA may be used to construct antisense sequences to control the
CC   expression of the coding sequence of interest. The agonists and
CC   antagonists are useful for treating otitis media, conjunctivitis,
CC   pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and
CC   endocarditis.
XX
SQ   Sequence 638 BP; 149 A; 140 C; 202 G; 147 T; 0 other;

  Query Match             4.5%;  Score 27;  DB 22;  Length 638;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
          |||||||||||||||||||||||||||
Db    296 TAGGAGGAGACCGCCCCAGTCAAACTA 270


RESULT 5
AAS82419
ID   AAS82419 standard; cDNA; 813 BP.
XX
AC   AAS82419;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #18223.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG18232.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 18223; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 813 BP; 200 A; 234 C; 187 G; 192 T; 0 other;

  Query Match             4.5%;  Score 27;  DB 23;  Length 813;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
          |||||||||||||||||||||||||||
Db    411 TAGGAGGAGACCGCCCCAGTCAAACTA 437
```

```
RESULT 6
AAK99200/c
ID   AAK99200 standard; RNA; 1258 BP.
XX
AC   AAK99200;
XX
DT   11-JUN-2002  (first entry)
XX
DE   1258nt of E-site RNA within E. coli rRNA.
XX
KW   RNA-binding; fluorescent reporter molecule; oxazolidinone; viral genome;
KW   aminoglycoside; internal ribosome entry site; IRES; E-site RNA; toxic;
KW   antibiotic; ss.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    2..5
FT                   /*tag= a
FT                   /bound_moiety= "Nucleotides 363-360 of itself"
FT                   /note= "Bound to nucleotides 363-360 of itself"
FT   misc_binding    10..17
FT                   /*tag= b
FT                   /bound_moiety= "Nucleotides 358-351 of itself"
FT                   /note= "Bound to nucleotides 358-351 of itself"
FT   misc_binding    19..20
FT                   /*tag= c
FT                   /bound_moiety= "Nucleotides 349-348 of itself"
FT                   /note= "Bound to nucleotides 349-348 of itself"
FT   stem_loop       36..60
FT                   /*tag= d
FT   stem_loop       62..104
FT                   /*tag= e
FT   misc_binding    106
FT                   /*tag= f
FT                   /bound_moiety= "Nucleotide 110 of itself"
FT                   /note= "Bound to nucleotide 110 of itself"
FT   misc_binding    110
FT                   /*tag= g
FT                   /bound_moiety= "Nucleotide 106 of itself"
FT                   /note= "Bound to nucleotide 106 of itself"
FT   misc_binding    118..122
FT                   /*tag= h
FT                   /bound_moiety= "Nucleotides 342-338 of itself"
FT                   /note= "Bound to nucleotides 342-338 of itself"
FT   misc_binding    125..126
FT                   /*tag= i
FT                   /bound_moiety= "Nucleotides 334-333 of itself"
FT                   /note= "Bound to nucleotides 334-333 of itself"
FT   stem_loop       129..143
FT                   /*tag= j
FT   stem_loop       146..181
FT                   /*tag= k
FT   stem_loop       189..259
FT                   /*tag= l
FT   stem_loop       260..278
FT                   /*tag= m
FT   stem_loop       281..298
FT                   /*tag= n
FT   stem_loop       299..315
FT                   /*tag= o
FT   misc_binding    348..349
FT                   /*tag= p
FT                   /bound_moiety= "Nucleotides 20-19 of itself"
FT                   /note= "Bound to nucleotides 20-19 of itself"
FT   misc_binding    351..358
FT                   /*tag= q
FT                   /bound_moiety= "Nucleotides 17-10 of itself"
FT                   /note= "Bound to nucleotides 17-10 of itself"
FT   misc_binding    360..363
FT                   /*tag= r
FT                   /bound_moiety= "Nucleotides 5-2 of itself"
FT                   /note= "Bound to nucleotides 5-2 of itself"
FT   stem_loop       377..394
FT                   /*tag= s
FT   misc_binding    397..404
FT                   /*tag= t
FT                   /bound_moiety= "Nucleotides 979-972 of itself"
FT                   /note= "Bound to nucleotides 979-972 of itself"
FT   misc_binding    406..408
FT                   /*tag= u
FT                   /bound_moiety= "Nucleotides 971-969 of itself"
FT                   /note= "Bound to nucleotides 971-969 of itself"
FT   misc_binding    410..411
FT                   /*tag= v
FT                   /bound_moiety= "Nucleotides 966-965 of itself"
FT                   /note= "Bound to nucleotides 966-965 of itself"
FT   misc_binding    417..421
FT                   /*tag= w
FT                   /bound_moiety= "Nucleotides 801-797 of itself"
FT                   /note= "Bound to nucleotides 801-797 of itself"
FT   misc_binding    423..424
FT                   /*tag= x
FT                   /bound_moiety= "Nucleotides 796-795 of itself"
FT                   /note= "Bound to nucleotides 796-795 of itself"
FT   misc_binding    425..429
FT                   /*tag= y
FT                   /bound_moiety= "Nucleotides 792-788 of itself"
FT                   /note= "Bound to nucleotides 792-788 of itself"
FT   misc_binding    431..434
FT                   /*tag= z
FT                   /bound_moiety= "Nucleotides 597-594 of itself"
FT                   /note= "Bound to nucleotides 597-594 of itself"
FT   misc_binding    438
FT                   /*tag= aa
FT                   /bound_moiety= "Nucleotide 589 of itself"
FT                   /note= "Bound to nucleotide 589 of itself"
FT   misc_binding    441..444
FT                   /*tag= ab
FT                   /bound_moiety= "Nucleotides 586-583 of itself"
FT                   /note= "Bound to nucleotides 586-583 of itself"
FT   misc_binding    447..452
FT                   /*tag= ac
FT                   /bound_moiety= "Nucleotides 550-545 of itself"
FT                   /note= "Bound to nucleotides 550-545 of itself"
FT   misc_binding    455..457
FT                   /*tag= ad
FT                   /bound_moiety= "Nucleotides 542-540 of itself"
FT                   /note= "Bound to nucleotides 542-540 of itself"
FT   misc_binding    459..460
FT                   /*tag= ae
FT                   /bound_moiety= "Nucleotides 538-537 of itself"
FT                   /note= "Bound to nucleotides 538-537 of itself"
FT   misc_binding    474..478
FT                   /*tag= af
FT                   /bound_moiety= "Nucleotides 532-528 of itself"
FT                   /note= "Bound to nucleotides 532-528 of itself"
FT   stem_loop       481..515
FT                   /*tag= ag
FT   misc_binding    528..532
FT                   /*tag= ah
FT                   /bound_moiety= "Nucleotides 478-474 of itself"
FT                   /note= "Bound to nucleotides 478-474 of itself"
FT   misc_binding    537..538
FT                   /*tag= ai
FT                   /bound_moiety= "Nucleotides 460-459 of itself"
FT                   /note= "Bound to nucleotides 460-459 of itself"
FT   misc_binding    540..542
FT                   /*tag= aj
FT                   /bound_moiety= "Nucleotides 457-455 of itself"
FT                   /note= "Bound to nucleotides 457-455 of itself"
FT   misc_binding    545..550
FT                   /*tag= ak
FT                   /bound_moiety= "Nucleotides 452-447 of itself"
FT                   /note= "Bound to nucleotides 452-447 of itself"
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FT   stem_loop       554..577
FT                   /*tag= al
FT   misc_binding    583..586
FT                   /*tag= am
FT                   /bound_moiety= "Nucleotides 444-441 of itself"
FT                   /note= "Bound to nucleotides 444-441 of itself"
FT   misc_binding    589
FT                   /*tag= an
FT                   /bound_moiety= "Nucleotide 438 of itself"
FT                   /note= "Bound to nucleotide 438 of itself"
FT   misc_binding    594..597
FT                   /*tag= ao
FT                   /bound_moiety= "Nucleotides 434-431 of itself"
FT                   /note= "Bound to nucleotides 434-431 of itself"
FT   stem_loop       600..612
FT                   /*tag= ap
FT   stem_loop       613..635
FT                   /*tag= aq
FT   misc_binding    642..649
FT                   /*tag= ar
FT                   /bound_moiety= "Nucleotides 698-691 of itself"
FT                   /note= "Bound to nucleotides 698-691 of itself"
FT   stem_loop       650..676
FT                   /*tag= as
FT   misc_binding    691..698
FT                   /*tag= at
FT                   /bound_moiety= "Nucleotides 649-642 of itself"
FT                   /note= "Bound to nucleotides 649-642 of itself"
FT   stem_loop       701..724
FT                   /*tag= au
FT   stem_loop       726..735
FT                   /*tag= av
FT   stem_loop       749..775
FT                   /*tag= aw
FT   misc_binding    788..792
FT                   /*tag= ax
FT                   /bound_moiety= "Nucleotides 434-431 of itself"
FT                   /note= "Bound to nucleotides 434-431 of itself"
FT   misc_binding    795..796
FT                   /*tag= ay
FT                   /bound_moiety= "Nucleotides 424-423 of itself"
FT                   /note= "Bound to nucleotides 424-423 of itself"
FT   misc_binding    797..801
FT                   /*tag= az
FT                   /bound_moiety= "Nucleotides 421-417 of itself"
FT                   /note= "Bound to nucleotides 421-417 of itself"
FT   stem_loop       809..850
FT                   /*tag= ba
FT   misc_binding    861
FT                   /*tag= bb
FT                   /bound_moiety= "Nucleotide 935 of itself"
FT                   /note= "Bound to nucleotide 935 of itself"
FT   misc_binding    863..865
FT                   /*tag= bc
FT                   /bound_moiety= "Nucleotides 933-931 of itself"
FT                   /note= "Bound to nucleotides 933-931 of itself"
FT   misc_binding    866

  Query Match             4.5%;  Score 27;  DB 24;  Length 1258;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
           |||||||||||||||||||||||||||
Db     620 TAGGAGGAGACCGCCCCAGTCAAACTA 594


RESULT 7
AAS87232/c
ID   AAS87232 standard; cDNA; 1446 BP.
XX
AC   AAS87232;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #23036.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG23045.
XX
PT   New isolated polynucleotide and.encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 23036; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1446 BP; 331 A; 354 C; 459 G; 302 T; 0 other;

  Query Match             4.5%;  Score 27;  DB 23;  Length 1446;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
           |||||||||||||||||||||||||||
Db     815 TAGGAGGAGACCGCCCCAGTCAAACTA 789


RESULT 8
AAS77887/c
ID   AAS77887 standard; cDNA; 2115 BP.
XX
AC   AAS77887;
XX
DT   13-FEB-2002  (first entry)
XX
```

DE DNA encoding novel human diagnostic protein #13691.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG13700.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 13691; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2115 BP; 389 A; 652 C; 728 G; 346 T; 0 other;

Query Match 4.5%; Score 27; DB 23; Length 2115;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
||||||||||||||||||||||||||||
Db 343 TAGGAGGAGACCGCCCCAGTCAAACTA 317

RESULT 9
AAA66047
ID AAA66047 standard; DNA; 2904 BP.
XX
AC AAA66047;
XX
DT 05-OCT-2000 (first entry)
XX
DE E. coli proliferation associated coding sequence SEQ ID NO:239.
XX
KW Escherichia coli; E. coli; proliferation; inhibition; screening;
KW antimicrobial; bacterial growth; antisense therapy; antibacterial; ds.
XX
OS Escherichia coli.
XX
PN WO200044906-A2.
XX
PD 03-AUG-2000.
XX
PF 27-JAN-2000; 2000WO-US02200.
XX
PR 27-JAN-1999; 99US-0117405.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Zyskind J, Ohlsen KL, Trawick J, Forsyth RA, Froelich JM, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2000-514822/46.
XX
PT Novel polynucleotides and polypeptides associated with microorganism
PT proliferation, used to identify inhibitors of bacterial growth and
PT proliferation, for use in antisense therapy -
XX
PS Claim 8; Page 172-173; 316pp; English.
XX
CC AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide
CC sequences derived from Escherichia coli which inhibit E. coli
CC proliferation. AAA65890 to AAA66055 and AAB15886 to AAB16040 represent
CC nucleotide and protein sequences associated with E. coli proliferation.
CC AAA66056 and AAA66057 represent primers used for sequencing E. coli
CC proliferation inhibiting nucleotide inserts in an example from the
CC present invention. Methods from the present invention can be used to
CC identify a proliferation- required gene in a microorganism, by contacting
CC a microorganism with a proliferation-required gene activity inhibitory
CC nucleic acid identified in another organism, and determining if
CC inhibition occurs in the second microorganism. The nucleic acid sequences
CC identified as being required for bacterial growth and proliferation, can
CC be used for antisense therapy for killing bacteria.
XX
SQ Sequence 2904 BP; 591 A; 912 C; 639 G; 762 T; 0 other;

Query Match 4.5%; Score 27; DB 21; Length 2904;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
||||||||||||||||||||||||||||
Db 639 TAGGAGGAGACCGCCCCAGTCAAACTA 665

RESULT 10
AAA66052
ID AAA66052 standard; RNA; 2904 BP.
XX
AC AAA66052;
XX
DT 05-OCT-2000 (first entry)
XX
DE E. coli proliferation associated nucleotide sequence SEQ ID NO:399.
XX
KW Escherichia coli; E. coli; proliferation; inhibition; screening;
KW antimicrobial; bacterial growth; antisense therapy; antibacterial; ss.
XX
OS Escherichia coli.
XX
PN WO200044906-A2.
XX
PD 03-AUG-2000.
XX
PF 27-JAN-2000; 2000WO-US02200.
XX
PR 27-JAN-1999; 99US-0117405.

```
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Zyskind J,  Ohlsen KL,  Trawick J,  Forsyth RA,  Froelich JM,  Carr GJ;
PI   Yamamoto RT,  Xu HH;
XX
DR   WPI; 2000-514822/46.
XX
PT   Novel polynucleotides and polypeptides associated with microorganism
PT   proliferation, used to identify inhibitors of bacterial growth and
PT   proliferation, for use in antisense therapy -
XX
PS   Example 3; Page 295-296; 316pp; English.
XX
CC   AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide
CC   sequences derived from Escherichia coli which inhibit E. coli
CC   proliferation. AAA65890 to AAA66055 and AAB15886 to AAB16040 represent
CC   nucleotide and protein sequences associated with E. coli proliferation.
CC   AAA66056 and AAA66057 represent primers used for sequencing E. coli
CC   proliferation inhibiting nucleotide inserts in an example from the
CC   present invention. Methods from the present invention can be used to
CC   identify a proliferation- required gene in a microorganism, by contacting
CC   a microorganism with a proliferation-required gene activity inhibitory
CC   nucleic acid identified in another organism, and determining if
CC   inhibition occurs in the second microorganism. The nucleic acid sequences
CC   identified as being required for bacterial growth and proliferation, can
CC   be used for antisense therapy for killing bacteria.
XX
SQ   Sequence 2904 BP; 591 A; 912 C; 639 G; 762 U; 0 other;

  Query Match             4.5%;  Score 27;  DB 21;  Length 2904;
  Best Local Similarity   88.9%;  Pred. No. 0.012;
  Matches   24;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
          :|||||||||||||||||||:|||||:|
Db    639 UAGGAGGAGACCGCCCCAGUCAAACUA 665


RESULT 11
AAH75411/c
ID   AAH75411 standard; rRNA; 2904 BP.
XX
AC   AAH75411;
XX
DT   22-OCT-2001  (first entry)
XX
DE   E. coli 23S rRNA.
XX
KW   16S rRNA; 23S rRNA; RNA binding; antimicrobial; ss.
XX
OS   Escherichia coli.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1..8
FT                   /*tag=  a
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 2902-2895 to form a duplex"
FT   misc_binding    16..24
FT                   /*tag=  b
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 525-516 to form a duplex"
FT   misc_binding    30
FT                   /*tag=  c
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotide 510"
FT   misc_binding    31..32
FT                   /*tag=  d
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 474-473 to form a duplex"
FT   misc_binding    35..44
FT                   /*tag=  e
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 445-433 to form a duplex"
FT   misc_binding    54..56
FT                   /*tag=  f
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 116-114 to form a duplex"
FT   stem_loop       58..69
FT                   /*tag=  g
FT   stem_loop       76..110
FT                   /*tag=  h
FT   misc_binding    114..116
FT                   /*tag=  i
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 56-54 to form a duplex"
FT   stem_loop       121..130
FT                   /*tag=  j
FT   stem_loop       131..148
FT                   /*tag=  k
FT   stem_loop       150..176
FT                   /*tag=  l
FT   stem_loop       184..212
FT                   /*tag=  m
FT   stem_loop       224..231
FT                   /*tag=  n
FT   stem_loop       235..262
FT                   /*tag=  o
FT   misc_binding    265..268
FT                   /*tag=  p
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 427-424 to form a duplex"
FT   misc_binding    271..297
FT                   /*tag=  q
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 366-341 to form a duplex"
FT   stem_loop       301..316
FT                   /*tag=  r
FT   stem_loop       319..323
FT                   /*tag=  s
FT   stem_loop       325..337
FT                   /*tag=  t
FT   misc_binding    341..366
FT                   /*tag=  u
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 297-271 to form a duplex"
FT   stem_loop       376..398
FT                   /*tag=  v
FT   stem_loop       406..421
FT                   /*tag=  w
FT   misc_binding    424..427
FT                   /*tag=  x
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 268-265 to form a duplex"
FT   misc_binding    433..445
FT                   /*tag=  y
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 44-35 to form a duplex"
FT   stem_loop       461..468
FT                   /*tag=  z
FT   misc_binding    473..474
FT                   /*tag=  aa
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 32-31 to form a duplex"
FT   stem_loop       484..496
FT                   /*tag=  ab
FT   misc_binding    510
FT                   /*tag=  ac
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotide 30"
FT   misc_binding    516..525
FT                   /*tag=  ad
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 24-16 to form a duplex"
FT   stem_loop       533..560
FT                   /*tag=  ae
```

```
FT   misc_binding    579..584
FT                   /*tag= af
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1261-1256 to form a duplex"
FT   misc_binding    589..601
FT                   /*tag= ag
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 668-656 to form a duplex"
FT   stem_loop       604..624
FT                   /*tag= ah
FT   stem_loop       628..635
FT                   /*tag= ai
FT   stem_loop       638..650
FT                   /*tag= aj
FT   misc_binding    656..668
FT                   /*tag= ak
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 601-589 to form a duplex"
FT   misc_binding    671..672
FT                   /*tag= al
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 809-808 to form a duplex"
FT   misc_binding    678..683
FT                   /*tag= am
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 799-794 to form a duplex"
FT   misc_binding    687..698
FT                   /*tag= an
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 763-775 to form a duplex"
FT   stem_loop       700..732
FT                   /*tag= ao
FT   stem_loop       736..760
FT                   /*tag= ap
FT   protein_bind    752
FT                   /*tag= aq
FT                   /bound_moiety= "Vemamycin B"
FT   misc_binding    763..775
FT                   /*tag= ar
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 698-687 to form a duplex"
FT   stem_loop       777..787
FT                   /*tag= as
FT   misc_binding    794..799
FT                   /*tag= at
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 683-678 to form a duplex"
FT   misc_binding    808..809
FT                   /*tag= au
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 672-671 to form a duplex"
FT   misc_binding    812..817
FT                   /*tag= av
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1195-1190 to form a duplex"
FT   stem_loop       822..835
FT                   /*tag= aw
FT   stem_loop       838..940
FT                   /*tag= ax
FT   protein_bind    913
FT                   /*tag= ay
FT                   /bound_moiety= "Viomycin"
FT   protein_bind    914
FT                   /*tag= az
FT                   /bound_moiety= "Viomycin"
FT   stem_loop       946..971
FT                   /*tag= ba
FT   stem_loop       976..987
FT                   /*tag= bb
FT   misc_binding    991..998
FT                   /*tag= bc
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1163-1157 to form a duplex"
FT   misc_binding    1002..1004
FT                   /*tag= bd
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1153-1151 to form a duplex"
FT   misc_binding    1011..1019
FT                   /*tag= be
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1150-1143 to form a duplex"
FT   misc_binding    1030..1043
FT                   /*tag= bf
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1124-1112 to form a duplex"
FT   misc_feature    1031..1123
FT                   /*tag= bg
FT                   /label= "GTPase Centre"
FT   misc_binding    1052..1055
FT                   /*tag= bh
FT                   /bound_moiety= "23S rRNA"
FT                   /note= "Binds nucleotides 1107-1104 to form a duplex"
FT   stem_loop       1057..1081
FT                   /*tag= bi
FT   protein_bind    1067

  Query Match             4.5%;  Score 27;  DB 22;  Length 2904;
  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
           |||||||||||||||||||||||||||
Db    2267 TAGGAGGAGACCGCCCCAGTCAAACTA 2241


RESULT 12
AAF23016/c
ID   AAF23016 standard; rRNA; 2904 BP.
XX
AC   AAF23016;
XX
DT   20-MAR-2001  (first entry)
XX
DE   E. coli 23S rRNA sequence.
XX
KW   Probe; PCR primer; 5S rRNA; 16S rRNA; 23S rRNA; 28S rRNA; 18S rRNA;
KW   Mycobacterium; Enterococcus; Chlamydia; Mycoplasma; E. coli; Legionella;
KW   Salmonella; Pseudomonas; Campylobacter; Neisseria gonorrheae; fungus;
KW   bacterium; ss.
XX
OS   Escherichia coli.
XX
PN   US6150517-A.
XX
PD   21-NOV-2000.
XX
PF   30-MAY-1995;   95US-0454063.
XX
PR   22-FEB-1994;   94US-0200866.
PR   24-NOV-1987;   87US-0295208.
PR   24-NOV-1987;   87WO-US03009.
PR   11-DEC-1991;   91US-0806929.
PR   24-NOV-1986;   86US-0934244.
PR   07-AUG-1987;   87US-0083542.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   McDonough SH,  Kop JA,  Smith RD,  Hogan JJ;
XX
DR   WPI; 2001-060029/07.
XX
PT   Preparing a probe for nucleic acid hybridization assays comprises
PT   constructing a nucleotide polymer sufficiently complementary to
PT   hybridize to an rRNA region that distinguishes non-viral target from
PT   non-viral non-target species -
XX
```

PS Disclosure; Fig 2; 75pp; English.
XX
CC The present invention provides novel methods of producing probes for use
CC in the identification of a number of microorganisms. These include E.
CC coli, Mycobacteria, Mycoplasma, Campylobacter, Chlamydia, Enterobacter,
CC Legionella, Salmonella, Pseudomonas, Neisseria gonorrheae, fungi and
CC bacteria.
XX
SQ Sequence 2904 BP; 762 A; 639 C; 912 G; 591 U; 0 other;

Query Match 4.5%; Score 27; DB 22; Length 2904;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
||||||||||||||||||||||||||||
Db 2266 TAGGAGGAGACCGCCCCAGTCAAACTA 2240

RESULT 13
AAC89403/c
ID AAC89403 standard; DNA; 2904 BP.
XX
AC AAC89403;
XX
DT 08-MAR-2001 (first entry)
XX
DE Sequences from 23S E.coli ribosomal RNA.
XX
KW 23S rRNA; ribosomal polynucleotide; infection; otitis media;
KW conjunctivitis; pneumonia; bacteremia; meningitis; sinusitis;
KW pleural empyema; endocarditis; ds.
XX
OS Escherichia coli.
XX
PN WO200071560-A1.
XX
PD 30-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-US12133.
XX
PR 20-MAY-1999; 99US-0134973.
PR 07-JUN-1999; 99US-0137837.
PR 14-JUN-1999; 99US-0139095.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Hegg LA, Sterner TA;
XX
DR WPI; 2001-102280/11.
XX
PT Novel bacterial ribosomal polynucleotides useful for identifying
PT agonists and antagonists for treating otitis media, conjunctivitis,
PT pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and
PT endocarditis -
XX
PS Claim 10; Page 18-19; 67pp; English.
XX
CC The present invention relates to Escherichia coli 23S rRNA.
CC Derivatives from this protein may be useful for treating an
CC individual having a need to inhibit a ribosomal polynucleotide.
CC Agonists and antagonists identified are useful for treating an
CC individual infected by Staphylococcus aureus or Streptococcus
CC pneumoniae. The DNA sequence may also be used in the
CC discovery and screening of antibacterial drugs, and its respective
CC mRNA may be used to construct antisense sequences to control the
CC expression of the coding sequence of interest. The agonists and
CC antagonists are useful for treating otitis media, conjunctivitis,
CC pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and
CC endocarditis.
XX
SQ Sequence 2904 BP; 762 A; 639 C; 912 G; 591 T; 0 other;

Query Match 4.5%; Score 27; DB 22; Length 2904;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
||||||||||||||||||||||||||||
Db 2266 TAGGAGGAGACCGCCCCAGTCAAACTA 2240

RESULT 14
AAV38096/c
ID AAV38096 standard; DNA; 2907 BP.
XX
AC AAV38096;
XX
DT 15-SEP-1998 (first entry)
XX
DE Enterohaemorrhagic E. coli 0157 23A rRNA gene DNA sequence.
XX
KW Enterohaemorrhagic; Escherichia coli 0157; 23S rRNA; hybridisation;
KW probe; detection; diagnosis; infection; PCR primer; ds.
XX
OS Escherichia coli.
XX
PN JP10165182-A.
XX
PD 23-JUN-1998.
XX
PF 09-DEC-1996; 96JP-0328837.
XX
PR 09-DEC-1996; 96JP-0328837.
XX
PA (NIFL-) NIPPON FLOUR MILLS CO LTD.
PA (ZENK-) ZENKOKU NOGYO KYODO KUMIAI RENGOKAI.
XX
DR WPI; 1998-416777/36.
XX
PT Hybridisation probe derived from 23S ribosomal RNA of
PT enterohaemorrhagic E. coli O157 - or the gene encoding the 23S
PT ribosomal RNA; used for the specific detection of enterohaemorrhagic
PT E. coli O157
XX
PS Example 2; Page 5-6; 18pp; Japanese.
XX
CC A method has been developed for the detection of enterohaemorrhagic
CC Escherichia coli (EHEC) O157 in which nucleic acid fragments of the
CC 23S ribosomal RNA (rRNA) gene from EHEC 0157 are used as hybridisation
CC probes. The present sequence represents the 23S rRNA gene from EHEC 0157
CC from the present invention. Probes from the present invention can be
CC labelled and used as hybridisation probes to detect EHEC O157 in a
CC sample. They can specifically detect E. coli O157 and hence diagnose
CC infection.
XX
SQ Sequence 2907 BP; 760 A; 638 C; 909 G; 592 T; 8 other;

Query Match 4.5%; Score 27; DB 19; Length 2907;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
||||||||||||||||||||||||||||
Db 2269 TAGGAGGAGACCGCCCCAGTCAAACTA 2243

RESULT 15
AAV38107/c
ID AAV38107 standard; rRNA; 2907 BP.
XX
AC AAV38107;
XX
DT 15-SEP-1998 (first entry)
XX

DE Enterohaemorrhagic E. coli 0157 23A rRNA gene rRNA sequence.
XX
KW Enterohaemorrhagic; Escherichia coli 0157; 23S rRNA; hybridisation;
KW probe; detection; diagnosis; infection; PCR primer; ss.
XX
OS Escherichia coli.
XX
PN JP10165182-A.
XX
PD 23-JUN-1998.
XX
PF 09-DEC-1996; 96JP-0328837.
XX
PR 09-DEC-1996; 96JP-0328837.
XX
PA (NIFL-) NIPPON FLOUR MILLS CO LTD.
PA (ZENK-) ZENKOKU NOGYO KYODO KUMIAI RENGOKAI.
XX
DR WPI; 1998-416777/36.
XX
PT Hybridisation probe derived from 23S ribosomal RNA of
PT enterohaemorrhagic E. coli O157 - or the gene encoding the 23S
PT ribosomal RNA; used for the specific detection of enterohaemorrhagic
PT E. coli O157
XX
PS Disclosure; Page 4-5; 18pp; Japanese.
XX
CC A method has been developed for the detection of enterohaemorrhagic
CC Escherichia coli (EHEC) O157 in which nucleic acid fragments of the
CC 23S ribosomal RNA (rRNA) gene from EHEC 0157 are used as hybridisation
CC probes. The present sequence represents the 23S rRNA gene from EHEC 0157
CC from the present invention. Probes from the present invention can be
CC labelled and used as hybridisation probes to detect EHEC O157 in a
CC sample. They can specifically detect E. coli O157 and hence diagnose
CC infection.
XX
SQ Sequence 2907 BP; 760 A; 638 C; 909 G; 592 U; 8 other;

Query Match 4.5%; Score 27; DB 19; Length 2907;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 287 TAGGAGGAGACCGCCCCAGTCAAACTA 313
||||||||||||||||||||||||||||
Db 2269 TAGGAGGAGACCGCCCCAGTCAAACTA 2243

Search completed: December 11, 2002, 20:39:05
Job time : 421 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 19:18:03 ; Search time 3172 Seconds
(without alignments)
5449.895 Million cell updates/sec

Title: US-09-369-992C-1_COPY_1147_1740
Perfect score: 594
Sequence: 1 gtatcgctttaataggcgaa.....ttacatctttcatgcaggtc 594

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
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7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
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22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	594	100.0	5849	3	PBU79731	U79731 Plasmodium
	2	497	83.7	2621	3	PBU79732	U79732 Plasmodium
	3	237	39.9	594	3	AF182847	AF182847 Plasmodiu
c	4	123	20.7	593	3	PMU97565	U97565 Plasmodium
c	5	123	20.7	594	3	PVU97561	U97561 Plasmodium
c	6	123	20.7	594	3	PVU97562	U97562 Plasmodium
c	7	117	19.7	594	3	PFU97559	U97559 Plasmodium
c	8	117	19.7	595	3	PFU97557	U97557 Plasmodium
c	9	117	19.7	595	3	PFU97558	U97558 Plasmodium
c	10	117	19.7	595	3	PFU97560	U97560 Plasmodium
c	11	117	19.7	596	3	PVU97563	U97563 Plasmodium
c	12	117	19.7	596	3	PVU97564	U97564 Plasmodium
c	13	117	19.7	598	3	PFU97556	U97556 Plasmodium
c	14	117	19.7	2700	3	PFLSRRN	X61660 Plasmodium
c	15	117	19.7	5142	3	PFTRNA	X75545 P.falciparu
c	16	117	19.7	15421	3	PFCOMPIRA	X95275 P.falciparu
	17	66	11.1	594	3	AF182846	AF182846 Plasmodiu
c	18	39	6.6	2700	3	AF304316	AF304316 Neospora
	19	39	6.6	3269	3	AF304322	AF304322 Neospora
c	20	39	6.6	4859	8	ANKCPRGOL	L42984 Ankistrodes
c	21	39	6.6	6113	3	TGTRNARRN	Y11430 T.gondii pl
c	22	39	6.6	7847	3	AF304319	AF304319 Neospora
	23	39	6.6	34996	3	U87145	U87145 Toxoplasma
c	24	39	6.6	34996	3	U87145	U87145 Toxoplasma
c	25	38	6.4	2558	8	MIQCPRGOL	L42847 Micromonas
c	26	35	5.9	2840	8	AF393596	AF393596 Entransia
c	27	33	5.6	117	8	PAV012608	AJ012608 Prunus av
c	28	33	5.6	238	8	CHCPRRNL4	X68908 Chloroplast
c	29	33	5.6	664	8	CHCMRRNL2	X68911 Chloroplast
c	30	33	5.6	675	8	CHCIRRNX5	X68897 Chloroplast
c	31	33	5.6	955	8	CHCKRRNL3	X68929 Chloroplast
c	32	33	5.6	957	8	CHCGRRNL2	X68892 Chloroplast
c	33	33	5.6	1064	8	PTERGD	L07260 Porphyra pu
c	34	33	5.6	1080	8	PTERGC	L07259 Porphyra pu
c	35	33	5.6	1130	8	OSU49840	U49840 Oryza sativ
c	36	33	5.6	1986	8	MZEMTCPAA	M36716 Maize mitoc
c	37	33	5.6	2524	8	CHCHRRNL1	X68921 Chloroplast
c	38	33	5.6	2552	8	TESCPRGOL	L42992 Tetraselmis
c	39	33	5.6	2568	8	SFCCPRGOL	L42854 Scourfieldi
c	40	33	5.6	2571	8	MEWCPRGOL	L49152 Mesostigma
c	41	33	5.6	2571	8	PDFCPRGOL	L42852 Pseudoscour
c	42	33	5.6	2572	8	CHCZRRNL1	X68919 Chloroplast
c	43	33	5.6	2603	8	CHCR7S3S	X16686 C. reinhard
c	44	33	5.6	2610	8	CMKCPRGOL	L42837 Chamaetrich
c	45	33	5.6	2619	8	URMCPRGOL	L42993 Uronema bel

ALIGNMENTS

RESULT 1
PBU79731
LOCUS PBU79731 5849 bp DNA linear INV 05-DEC-1997
DEFINITION Plasmodium berghei extrachromosomal plastid PB-1, ORF470 gene, partial cds, tRNA-Thr, large subunit ribosomal RNA, tRNA-Met, tRNA-Arg, tRNA-Val, tRNA-Arg, tRNA-Leu, tRNA-Asn, tRNA-Ala, and small subunit ribosomal RNA genes, complete sequences.
ACCESSION U79731
VERSION U79731.1 GI:2662401
KEYWORDS .
SOURCE Plasmodium berghei.
ORGANISM Plasmodium berghei
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 5849)
AUTHORS Yap,M.W., Kara,U.A., ten Heggeler-Bordier,B., Ting,R.C. and

```
            Tan,T.M.
  TITLE     Partial nucleotide sequence and organisation of extrachromosomal
            plastid-like DNA in Plasmodium berghei
  JOURNAL   Gene 200 (1-2), 91-98 (1997)
  MEDLINE   98038979
   PUBMED   9373142
REFERENCE   2  (bases 1 to 5849)
  AUTHORS   Yap,M.W.C., Kara,U.A.K. and Tan,T.M.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-NOV-1996) Institute of Molecular and Cell Biology,
            National University of Singapore, 10 Kent Ridge Crescent S119260,
            Singapore
FEATURES             Location/Qualifiers
     source          1. .5849
                     /organism="Plasmodium berghei"
                     /strain="ANKA"
                     /db_xref="taxon:5821"
                     /note="extrachromosomal plastid PB-1"
     CDS             complement(<1. .711)
                     /note="ORF470"
                     /codon_start=1
                     /protein_id="AAB88271.1"
                     /db_xref="GI:2662402"
                     /translation="MINKLKLKKFLNIYNLNYKYQYNNKINLYLIRNGLNKNLIKNLS
                     NNIYLYFFIYKFKIYSLKFLNMFKLPDWSCFECPNISYDNIIYYSSTLKDSNLLVYLK
                     TNLNINFLDTYFNKKIIPIDVICDSISVLHTTQYFLKKLGIIFLSLLDVILKYPLLVK
                     KYLGTVVSYKDNFFANINSIIFSEGSFCYVSKYIKCSFNLSTYFKTNSYDFAQFERTL
                     LIASEFAYVGYLEGCTASL"
     tRNA            complement(739. .809)
                     /product="tRNA-Thr"
     rRNA            complement(814. .3521)
                     /product="large subunit ribosomal RNA"
     tRNA            complement(3565. .3636)
                     /product="tRNA-Met"
     tRNA            complement(3646. .3717)
                     /product="tRNA-Arg"
     tRNA            3742. .3813
                     /product="tRNA-Val"
     tRNA            3817. .3888
                     /product="tRNA-Arg"
     tRNA            3895. .3975
                     /product="tRNA-Leu"
     tRNA            complement(3996. .4058)
                     /product="tRNA-Asn"
     tRNA            4089. .4159
                     /product="tRNA-Ala"
     rRNA            4208. .5648
                     /product="small subunit ribosomal RNA"
     tRNA            5793. .5849
                     /product="tRNA-Ile"
BASE COUNT     2296 a    673 c    557 g   2323 t
ORIGIN

  Query Match           100.0%;  Score 594;  DB 3;  Length 5849;
  Best Local Similarity  100.0%;  Pred. No. 2.8e-284;
  Matches  594;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTATCGCTTTAATAGGCGAACAGACTTACCCTTAAAACATACTACTGCCTTAGGATGCGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1147 GTATCGCTTTAATAGGCGAACAGACTTACCCTTAAAACATACTACTGCCTTAGGATGCGA 1206

Qy      61 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAAGATTAGCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1207 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAAGATTAGCC 1266

Qy     121 TGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTATTAAATAATTATCG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1267 TGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTATTAAATAATTATCG 1326

Qy     181 GATCATTAAGACCGACATTAATCTCTGTTTAATTTGTAAATTTTACAGTTAATTATATAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1327 GATCATTAAGACCGACATTAATCTCTGTTTAATTTGTAAATTTTACAGTTAATTATATAT 1386

Qy     241 TTATCTTTATATAATAAATATAACATTGTACACCTCCGTTTTTATATAGGAGGAGACCGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1387 TTATCTTTATATAATAAATATAACATTGTACACCTCCGTTTTTATATAGGAGGAGACCGC 1446

Qy     301 CCCAGTCAAACTATCTTATAAATATTGTTAAAAATTTTGTTATAAAAATTTTATAAGAAT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1447 CCCAGTCAAACTATCTTATAAATATTGTTAAAAATTTTGTTATAAAAATTTTATAAGAAT 1506

Qy     361 TTATATATATATAAAATGGTATTTCATTAACAATTACATTATTTCCAAAAAAATAATATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1507 TTATATATATATAAAATGGTATTTCATTAACAATTACATTATTTCCAAAAAAATAATATT 1566

Qy     421 ACTACTTCCCATTTATTCTATGTTATATATATATATTTTCAATATCTATTAATAGTAAAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1567 ACTACTTCCCATTTATTCTATGTTATATATATATATTTTCAATATCTATTAATAGTAAAG 1626

Qy     481 CTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGCATCTTCACAGATAATTTTATTT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1627 CTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGCATCTTCACAGATAATTTTATTT 1686

Qy     541 CATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAGGTC 594
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1687 CATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAGGTC 1740


RESULT 2
PBU79732
LOCUS       PBU79732                2621 bp    DNA     linear   INV 05-DEC-1997
DEFINITION  Plasmodium berghei extrachromosomal plastid PB-2, tRNA-Pro,
            tRNA-Glu, tRNA-Lys, tRNA-Asp, tRNA-Ser, tRNA-Tyr, tRNA-Met,
            tRNA-Leu, tRNA-Cys, and tRNA-His genes, complete sequence, rps4
            gene, complete cds, tRNA-Thr gene, complete sequence, and large
            subunit ribosomal RNA gene, partial sequence.
ACCESSION   U79732
VERSION     U79732.1  GI:2662403
KEYWORDS    .
SOURCE      Plasmodium berghei.
  ORGANISM  Plasmodium berghei
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 2621)
  AUTHORS   Yap,M.W., Kara,U.A., ten Heggeler-Bordier,B., Ting,R.C. and
            Tan,T.M.
  TITLE     Partial nucleotide sequence and organisation of extrachromosomal
            plastid-like DNA in Plasmodium berghei
  JOURNAL   Gene 200 (1-2), 91-98 (1997)
  MEDLINE   98038979
   PUBMED   9373142
REFERENCE   2  (bases 1 to 2621)
  AUTHORS   Yap,M.W.C., Kara,U.A.K. and Tan,T.M.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-NOV-1996) Institute of Molecular and Cell Biology,
            National University of Singapore, 10 Kent Ridge Crescent S119260,
            Singapore
FEATURES             Location/Qualifiers
     source          1. .2621
                     /organism="Plasmodium berghei"
                     /strain="ANKA"
                     /db_xref="taxon:5821"
                     /note="extrachromosomal plastid PB-2"
     tRNA            complement(2. .73)
                     /product="tRNA-Pro"
     tRNA            complement(91. .160)
                     /product="tRNA-Glu"
     tRNA            complement(172. .240)
                     /product="tRNA-Lys"
     tRNA            complement(250. .324)
                     /product="tRNA-Asp"
     tRNA            complement(336. .422)
                     /product="tRNA-Ser"
     tRNA            complement(432. .516)
                     /product="tRNA-Tyr"
     tRNA            complement(521. .607)
                     /product="tRNA-Met"
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     tRNA            complement(join(617. .666,841. .876))
                     /product="tRNA-Leu"
     tRNA            complement(892. .963)
                     /product="tRNA-Cys"
     tRNA            complement(978. .1051)
                     /product="tRNA-His"
     CDS             complement(1066. .1689)
                     /codon_start=1
                     /product="rps4"
                     /protein_id="AAB88272.1"
                     /db_xref="GI:2662404"
                     /translation="MIKFLTPKIKMLKKLNLPFLLYLSSKYNYKLKINKYVYQSYFDL
                     KLKFVRYICYNYGITFKPYLHYLKKIQSHHENHLYLKLLNLLEPRLDVFLVNMGFLKL
                     YTTLRYYIRYKYVYLNKVYGNYYNIKLKGKDIIFFNKKIKYIISPNLIYRYNIYIYIS
                     NLYKYNFIKSSSFNDNFIICIYNFKIKILNDLYLNNILYIYNNIYNI"
     tRNA            complement(1717. .1789)
                     /product="tRNA-Thr"
     rRNA            complement(1803. .>2621)
                     /product="large subunit ribosomal RNA"
BASE COUNT     1035 a    327 c    229 g   1030 t
ORIGIN

  Query Match             83.7%;  Score 497;  DB 3;  Length 2621;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-236;
  Matches  497;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GTATCGCTTTAATAGGCGAACAGACTTACCCTTAAAACATACTACTGCCTTAGGATGCGA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2125 GTATCGCTTTAATAGGCGAACAGACTTACCCTTAAAACATACTACTGCCTTAGGATGCGA 2184

Qy      61 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAAGATTAGCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2185 TAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGAAAAGATTAGCC 2244

Qy     121 TGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTATTAAATAATTATCG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2245 TGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTATTAAATAATTATCG 2304

Qy     181 GATCATTAAGACCGACATTAATCTCTGTTTAATTTGTAAATTTTACAGTTAATTATATAT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2305 GATCATTAAGACCGACATTAATCTCTGTTTAATTTGTAAATTTTACAGTTAATTATATAT 2364

Qy     241 TTATCTTTATATAATAAATATAACATTGTACACCTCCGTTTTTATATAGGAGGAGACCGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2365 TTATCTTTATATAATAAATATAACATTGTACACCTCCGTTTTTATATAGGAGGAGACCGC 2424

Qy     301 CCCAGTCAAACTATCTTATAAATATTGTTAAAAATTTTGTTATAAAAATTTTATAAGAAT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2425 CCCAGTCAAACTATCTTATAAATATTGTTAAAAATTTTGTTATAAAAATTTTATAAGAAT 2484

Qy     361 TTATATATATATAAAATGGTATTTCATTAACAATTACATTATTTCCAAAAAAATAATATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2485 TTATATATATATAAAATGGTATTTCATTAACAATTACATTATTTCCAAAAAAATAATATT 2544

Qy     421 ACTACTTCCCATTTATTCTATGTTATATATATATATTTTCAATATCTATTAATAGTAAAG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2545 ACTACTTCCCATTTATTCTATGTTATATATATATATTTTCAATATCTATTAATAGTAAAG 2604

Qy     481 CTTCATAGGGTCTTTCT 497
          |||||||||||||||||
Db    2605 CTTCATAGGGTCTTTCT 2621


RESULT 3
AF182847
LOCUS       AF182847                 594 bp    DNA     linear   INV 25-OCT-1999
DEFINITION  Plasmodium chabaudi from Australia large subunit ribosomal RNA
            gene, partial sequence.
ACCESSION   AF182847
VERSION     AF182847.1  GI:6110458
KEYWORDS    .
SOURCE      Plasmodium chabaudi.
  ORGANISM  Plastid Plasmodium chabaudi
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Tham,J.M., Khoh,L.K. and Kara,A.U.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1999) Institute of Molecular and Cell Biology, 30
            Medical Drive, Singapore 117609, Singapore
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Plasmodium chabaudi"
                     /organelle="plastid"
                     /strain="adami DS"
                     /db_xref="taxon:5825"
                     /country="Australia"
     rRNA            <1. .>594
                     /product="large subunit ribosomal RNA"
BASE COUNT      205 a     95 c     69 g    225 t
ORIGIN

  Query Match             39.9%;  Score 237;  DB 3;  Length 594;
  Best Local Similarity   99.4%;  Pred. No. 7.9e-107;
  Matches  337;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      50 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      50 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 109

Qy     110 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTATTA 169
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     110 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATCTTATTATTA 169

Qy     170 AATAATTATCGGATCATTAAGACCGACATTAATCTCTGTTTAATTTGTAAATTTTACAGT 229
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     170 AATAATTATCGGATCATTAAGACCGACATTAATCTCTGTTTAATTTGTAAATTTTACAGT 229

Qy     230 TAATTATATATTTATCTTTATATAATAAATATAACATTGTACACCTCCGTTTTTATATAG 289
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     230 TAATTATATATTTATCTTTATATAATAAATATAACATTGTACACCTCCGTTTTTATATAG 289

Qy     290 GAGGAGACCGCCCCAGTCAAACTATCTTATAAATATTGTTAAAAATTTTGTTATAAAAAT 349
           |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     290 GAGGAGACCGCCCCAGTCAAACTATCTTATAAATATTGTAAAAAATTTTGTTATAAAAAT 349

Qy     350 TTTATAAGAATTTATATATATATAAAATGGTATTTCATT 388
           |||||||||||||||||||||||||||||||||||||||
Db     350 TTTATAAGAATTTATATATATATAAAATGGTATTTCATT 388


RESULT 4
PMU97565/c
LOCUS       PMU97565                 593 bp    DNA     linear   INV 15-MAR-2001
DEFINITION  Plasmodium malariae extrachromosomal plastid large subunit
            ribosomal RNA gene, partial sequence.
ACCESSION   U97565
VERSION     U97565.1  GI:4100403
KEYWORDS    .
SOURCE      Plasmodium malariae.
  ORGANISM  Plasmodium malariae
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 593)
  AUTHORS   Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
  TITLE     Direct PCR amplification and sequence analysis of extrachromosomal
            Plasmodium DNA from dried blood spots
  JOURNAL   Acta Trop. 68 (1), 105-114 (1997)
  MEDLINE   98013247
   PUBMED   9352006
REFERENCE   2  (bases 1 to 593)
  AUTHORS   Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
            National University of Singapore, 10 Kent Ridge Crescent S119260,
            Singapore
FEATURES             Location/Qualifiers
     source          1. .593
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                     /organism="Plasmodium malariae"
                     /isolate="primary isolate pv16/1"
                     /db_xref="taxon:5858"
                     /note="extrachromosomal plastid"
     rRNA            <1. .>593
                     /product="large subunit ribosomal RNA"
BASE COUNT      227 a     70 c     98 g    198 t
ORIGIN

  Query Match             20.7%;  Score 123;  DB 3;  Length 593;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-50;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    472 ATAGTAAAGCTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGCATCTTCACAGATA 531
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 ATAGTAAAGCTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGCATCTTCACAGATA 64

Qy    532 ATTTTATTTCATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAG 591
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 ATTTTATTTCATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAG 4

Qy    592 GTC 594
          |||
Db      3 GTC 1


RESULT 5
PVU97561/c
LOCUS       PVU97561                  594 bp    DNA     linear   INV 15-MAR-2001
DEFINITION  Plasmodium vivax extrachromosomal plastid large subunit ribosomal
            RNA gene, partial sequence.
ACCESSION   U97561
VERSION     U97561.1  GI:4100399
KEYWORDS    .
SOURCE      Plasmodium vivax.
  ORGANISM  Plasmodium vivax
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
  TITLE     Direct PCR amplification and sequence analysis of extrachromosomal
            Plasmodium DNA from dried blood spots
  JOURNAL   Acta Trop. 68 (1), 105-114 (1997)
  MEDLINE   98013247
   PUBMED   9352006
REFERENCE   2  (bases 1 to 594)
  AUTHORS   Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
            National University of Singapore, 10 Kent Ridge Crescent S119260,
            Singapore
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Plasmodium vivax"
                     /isolate="primary isolate pv12/p"
                     /db_xref="taxon:5855"
                     /note="extrachromosomal plastid"
     rRNA            <1. .>594
                     /product="large subunit ribosomal RNA"
BASE COUNT      227 a     70 c     98 g    199 t
ORIGIN

  Query Match             20.7%;  Score 123;  DB 3;  Length 594;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-50;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    472 ATAGTAAAGCTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGCATCTTCACAGATA 531
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 ATAGTAAAGCTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGCATCTTCACAGATA 64

Qy    532 ATTTTATTTCATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAG 591
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 ATTTTATTTCATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAG 4

Qy    592 GTC 594
          |||
Db      3 GTC 1


RESULT 6
PVU97562/c
LOCUS       PVU97562                  594 bp    DNA     linear   INV 15-MAR-2001
DEFINITION  Plasmodium vivax extrachromosomal plastid large subunit ribosomal
            RNA gene, partial sequence.
ACCESSION   U97562
VERSION     U97562.1  GI:4100400
KEYWORDS    .
SOURCE      Plasmodium vivax.
  ORGANISM  Plasmodium vivax
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
  TITLE     Direct PCR amplification and sequence analysis of extrachromosomal
            Plasmodium DNA from dried blood spots
  JOURNAL   Acta Trop. 68 (1), 105-114 (1997)
  MEDLINE   98013247
   PUBMED   9352006
REFERENCE   2  (bases 1 to 594)
  AUTHORS   Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
            National University of Singapore, 10 Kent Ridge Crescent S119260,
            Singapore
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Plasmodium vivax"
                     /isolate="primary isolate pv13/p"
                     /db_xref="taxon:5855"
                     /note="extrachromosomal plastid"
     rRNA            <1. .>594
                     /product="large subunit ribosomal RNA"
BASE COUNT      225 a     72 c     99 g    198 t
ORIGIN

  Query Match             20.7%;  Score 123;  DB 3;  Length 594;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-50;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    472 ATAGTAAAGCTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGCATCTTCACAGATA 531
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 ATAGTAAAGCTTCATAGGGTCTTTCTGTCCTAATATAAGAAATCTGCATCTTCACAGATA 64

Qy    532 ATTTTATTTCATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAG 591
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 ATTTTATTTCATTAAGATTTTTTTTAAGACAGCATTTAAGTCGTTACATCTTTCATGCAG 4

Qy    592 GTC 594
          |||
Db      3 GTC 1


RESULT 7
PFU97559/c
LOCUS       PFU97559                  594 bp    DNA     linear   INV 15-MAR-2001
DEFINITION  Plasmodium falciparum extrachromosomal plastid large subunit
            ribosomal RNA gene, partial sequence.
ACCESSION   U97559
VERSION     U97559.1  GI:4100397
KEYWORDS    .
SOURCE      Plasmodium falciparum.
  ORGANISM  Plasmodium falciparum
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
  TITLE     Direct PCR amplification and sequence analysis of extrachromosomal
            Plasmodium DNA from dried blood spots
  JOURNAL   Acta Trop. 68 (1), 105-114 (1997)
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  MEDLINE   98013247
   PUBMED   9352006
REFERENCE   2  (bases 1 to 594)
  AUTHORS   Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
            National University of Singapore, 10 Kent Ridge Crescent S119260,
            Singapore
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Plasmodium falciparum"
                     /isolate="primary isolate pf20/1"
                     /db_xref="taxon:5833"
                     /note="extrachromosomal plastid"
     rRNA            <1. .>594
                     /product="large subunit ribosomal RNA"
BASE COUNT      231 a     71 c     90 g    202 t
ORIGIN

  Query Match             19.7%;  Score 117;  DB 3;  Length 594;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-47;
  Matches  117;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      50 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     545 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 486

Qy     110 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     485 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 429


RESULT 8
PFU97557/c
LOCUS       PFU97557                595 bp    DNA     linear   INV 15-MAR-2001
DEFINITION  Plasmodium falciparum extrachromosomal plastid large subunit
            ribosomal RNA gene, partial sequence.
ACCESSION   U97557
VERSION     U97557.1  GI:4100395
KEYWORDS    .
SOURCE      Plasmodium falciparum.
  ORGANISM  Plasmodium falciparum
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
  TITLE     Direct PCR amplification and sequence analysis of extrachromosomal
            Plasmodium DNA from dried blood spots
  JOURNAL   Acta Trop. 68 (1), 105-114 (1997)
  MEDLINE   98013247
   PUBMED   9352006
REFERENCE   2  (bases 1 to 595)
  AUTHORS   Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
            National University of Singapore, 10 Kent Ridge Crescent S119260,
            Singapore
FEATURES             Location/Qualifiers
     source          1. .595
                     /organism="Plasmodium falciparum"
                     /isolate="primary isolate pf11/p"
                     /db_xref="taxon:5833"
                     /note="extrachromosomal plastid"
     rRNA            <1. .>595
                     /product="large subunit ribosomal RNA"
BASE COUNT      229 a     77 c     93 g    196 t
ORIGIN

  Query Match             19.7%;  Score 117;  DB 3;  Length 595;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-47;
  Matches  117;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      50 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 109
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RESULT 9
PFU97558/c
LOCUS       PFU97558                595 bp    DNA     linear   INV 15-MAR-2001
DEFINITION  Plasmodium falciparum extrachromosomal plastid large subunit
            ribosomal RNA gene, partial sequence.
ACCESSION   U97558
VERSION     U97558.1  GI:4100396
KEYWORDS    .
SOURCE      Plasmodium falciparum.
  ORGANISM  Plasmodium falciparum
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
  TITLE     Direct PCR amplification and sequence analysis of extrachromosomal
            Plasmodium DNA from dried blood spots
  JOURNAL   Acta Trop. 68 (1), 105-114 (1997)
  MEDLINE   98013247
   PUBMED   9352006
REFERENCE   2  (bases 1 to 595)
  AUTHORS   Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
            National University of Singapore, 10 Kent Ridge Crescent S119260,
            Singapore
FEATURES             Location/Qualifiers
     source          1. .595
                     /organism="Plasmodium falciparum"
                     /isolate="primary isolate pf19/i"
                     /db_xref="taxon:5833"
                     /note="extrachromosomal plastid"
     rRNA            <1. .>595
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BASE COUNT      233 a     72 c     89 g    201 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.6e-47;
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Qy      50 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 109
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Qy     110 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     486 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 430


RESULT 10
PFU97560/c
LOCUS       PFU97560                595 bp    DNA     linear   INV 15-MAR-2001
DEFINITION  Plasmodium falciparum extrachromosomal plastid large subunit
            ribosomal RNA gene, partial sequence.
ACCESSION   U97560
VERSION     U97560.1  GI:4100398
KEYWORDS    .
SOURCE      Plasmodium falciparum.
  ORGANISM  Plasmodium falciparum
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
  TITLE     Direct PCR amplification and sequence analysis of extrachromosomal
            Plasmodium DNA from dried blood spots
  JOURNAL   Acta Trop. 68 (1), 105-114 (1997)
  MEDLINE   98013247
   PUBMED   9352006
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REFERENCE   2  (bases 1 to 595)
  AUTHORS   Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
            National University of Singapore, 10 Kent Ridge Crescent S119260,
            Singapore
FEATURES             Location/Qualifiers
     source          1. .595
                     /organism="Plasmodium falciparum"
                     /isolate="primary isolate pf18/s"
                     /db_xref="taxon:5833"
                     /note="extrachromosomal plastid"
     rRNA            <1. .>595
                     /product="large subunit ribosomal RNA"
BASE COUNT      231 a     71 c     91 g    202 t
ORIGIN

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Qy      50 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 109
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Db     546 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 487

Qy     110 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     486 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 430


RESULT 11
PVU97563/c
LOCUS       PVU97563                 596 bp    DNA     linear   INV 15-MAR-2001
DEFINITION  Plasmodium vivax extrachromosomal plastid large subunit ribosomal
            RNA gene, partial sequence.
ACCESSION   U97563
VERSION     U97563.1  GI:4100401
KEYWORDS    .
SOURCE      Plasmodium vivax.
  ORGANISM  Plasmodium vivax
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 596)
  AUTHORS   Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
  TITLE     Direct PCR amplification and sequence analysis of extrachromosomal
            Plasmodium DNA from dried blood spots
  JOURNAL   Acta Trop. 68 (1), 105-114 (1997)
  MEDLINE   98013247
   PUBMED   9352006
REFERENCE   2  (bases 1 to 596)
  AUTHORS   Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
            National University of Singapore, 10 Kent Ridge Crescent S119260,
            Singapore
FEATURES             Location/Qualifiers
     source          1. .596
                     /organism="Plasmodium vivax"
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BASE COUNT      232 a     72 c     90 g    202 t
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Qy      50 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 109
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Db     546 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 487

Qy     110 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     486 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 430


RESULT 12
PVU97564/c
LOCUS       PVU97564                 596 bp    DNA     linear   INV 15-MAR-2001
DEFINITION  Plasmodium vivax extrachromosomal plastid large subunit ribosomal
            RNA gene, partial sequence.
ACCESSION   U97564
VERSION     U97564.1  GI:4100402
KEYWORDS    .
SOURCE      Plasmodium vivax.
  ORGANISM  Plasmodium vivax
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 596)
  AUTHORS   Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
  TITLE     Direct PCR amplification and sequence analysis of extrachromosomal
            Plasmodium DNA from dried blood spots
  JOURNAL   Acta Trop. 68 (1), 105-114 (1997)
  MEDLINE   98013247
   PUBMED   9352006
REFERENCE   2  (bases 1 to 596)
  AUTHORS   Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
            National University of Singapore, 10 Kent Ridge Crescent S119260,
            Singapore
FEATURES             Location/Qualifiers
     source          1. .596
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                     /db_xref="taxon:5855"
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BASE COUNT      232 a     71 c     90 g    203 t
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Qy      50 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 109
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Db     546 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 487

Qy     110 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     486 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 430


RESULT 13
PFU97556/c
LOCUS       PFU97556                 598 bp    DNA     linear   INV 15-MAR-2001
DEFINITION  Plasmodium falciparum extrachromosomal plastid large subunit
            ribosomal RNA gene, partial sequence.
ACCESSION   U97556
VERSION     U97556.1  GI:4100394
KEYWORDS    .
SOURCE      Plasmodium falciparum.
  ORGANISM  Plasmodium falciparum
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 598)
  AUTHORS   Tan,T.M., Nelson,J.S., Ng,H.C., Ting,R.C. and Kara,U.A.
  TITLE     Direct PCR amplification and sequence analysis of extrachromosomal
            Plasmodium DNA from dried blood spots
  JOURNAL   Acta Trop. 68 (1), 105-114 (1997)
  MEDLINE   98013247
   PUBMED   9352006
REFERENCE   2  (bases 1 to 598)
  AUTHORS   Tan,T.M.C., Nelson,J.S., Ng,H.C., Ting,R.C.Y. and Kara,U.A.K.
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  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1997) Institute of Molecular and Cell Biology,
            National University of Singapore, 10 Kent Ridge Crescent S119260,
            Singapore
FEATURES             Location/Qualifiers
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Qy     110 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 166
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Db     489 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 433


RESULT 14
PFLSRRN/c
LOCUS       PFLSRRN                 2700 bp    DNA     linear   INV 27-SEP-1995
DEFINITION  Plasmodium falciparum gene for a large subunit ribosomal RNA from
            the inverted repeat within the 35-Kb circular DNA.
ACCESSION   X61660
VERSION     X61660.1  GI:13318
KEYWORDS    inverted repeat; ribosomal RNA; ribosomal RNA large subunit.
SOURCE      Plasmodium falciparum.
  ORGANISM  Plasmodium falciparum
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 2700)
  AUTHORS   Gardner,M.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-AUG-1991) M.J. Gardner, Div of Parasitology, National
            Inst for Medical Research, The Ridgeway - Mill Hill, London NW7
            1AA, UK
REFERENCE   2  (bases 1 to 2700)
  AUTHORS   Gardner,M.J., Feagin,J.E., Moore,D.J., Rangachari,K.,
            Williamson,D.H. and Wilson,R.J.
  TITLE     Sequence and organization of large subunit rRNA genes from the
            extrachromosomal 35 kb circular DNA of the malaria parasite
            Plasmodium falciparum
  JOURNAL   Nucleic Acids Res. 21 (5), 1067-1071 (1993)
  MEDLINE   93219063
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FEATURES             Location/Qualifiers
     source          1. .2700
                     /organism="Plasmodium falciparum"
                     /strain="C10"
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                     /dev_stage="Erythrocytic"
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ORIGIN

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Qy      50 TTAGGATGCGATAAGCCGACATCGAGGTGCCAAACCTTTTCGTCAATATGGACTCTCGGA 109
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Qy     110 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 166
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Db    2267 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 2211


RESULT 15
PFTRNA/c
LOCUS       PFTRNA                  5142 bp    DNA     circular INV 01-AUG-1994
DEFINITION  P.falciparum gene for tRNA I,A,N,L,R,V,R,M,T.
ACCESSION   X75545
VERSION     X75545.1  GI:520908
KEYWORDS    large ribosomal subunit; small ribosomal subunit RNA; transfer
            RNA-Ala; transfer RNA-Arg; transfer RNA-Asn; transfer RNA-Ile;
            transfer RNA-Leu; transfer RNA-Thr; transfer RNA-Val; trnA gene;
            trnI gene; trnL gene; trnM gene; trnN gene; trnR gene; trnT gene;
            trnV gene.
SOURCE      Plasmodium falciparum.
  ORGANISM  Plasmodium falciparum
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 5142)
  AUTHORS   Gardner,M., Preiser,P., Rangachari,K., Moore,D., Feagin,D.,
            Williamson,D.H. and Wilson,R.J.
  TITLE     Nine duplicated tRNA genes on the plastid-like DNA of the malaria
            parasite Plasmodium falciparum
  JOURNAL   Gene 140, 307-308 (1994)
REFERENCE   2  (bases 1 to 5142)
  AUTHORS   Wilson,R.J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-1993) R.J.M. Wilson, National Institute for
            MEdical Research, Mill Hill, London NW7 1AA, UK
FEATURES             Location/Qualifiers
     source          1. .5142
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                     /strain="BW (C10)"
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Qy     110 AAAGATTAGCCTGTTATCCCTAGAGTAACTTTTATCCGTTAAGCGATAATTTTATTA 166
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ARTICLES

tRNA genes transcribed from the plastid-like DNA of Plasmodium falciparum

P Preiser, DH Williamson and RJ Wilson

Division of Parasitology, National Institute for Medical Research, Mill Hill, London, UK.

Besides their mitochondrial genome, malarial parasites contain a second organellar DNA. This 35 kb circular molecule has a number of features reminiscent of plastid DNAs. Sequence analysis shows that along with other genes the circle codes for 25 different tRNAs all of which are transcribed. Six of the tRNAs have some unusual features, and one has an intron, the only one found so far on the circle. Comparison of codon and anticodon usage indicates that the 25 tRNAs are sufficient to decode all the protein genes present on the circle. The maintenance of such a parsimonious but complete translation system is further evidence for the functionality of the circle.

1: J Hepatol 1997 Oct;27(4):688-98 Related Articl

ELSEVIER SCIENCE FULL-TEXT ARTICLE

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Identification of human liver carboxylesterase of the proteins involved in Plasmodium falcipar malaria sporozoite invasion in primary cultures human hepatocytes.

van Pelt JF, Moshage HJ, Depla E, Verhave JP, Yap

Department of Liver and Pancreatic Diseases, Universit Hospital Gasthuisberg, Leuven, Belgium.

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BACKGROUND/AIMS: In a previous study, we have demonstrated that primary human hepatocytes in cultur susceptible for Plasmodium falciparum sporozoite invasi for development of parasites into exo-erythrocytic fori separate study we demonstrated the involvement of tw liver plasma membrane proteins (55 kD and 20 kD) in th invasion of P. falciparum sporozoites in vitro. In this stu have unravelled the nature of the 55 kD protein. METH For the identification of this protein, a 53-58 kD memb protein fraction from human liver was isolated, radioact labelled, incubated with sporozoites and cross-linked. A reduction of the cross-linker, the released proteins wer with unlabelled 53-58 kD protein fraction and separate

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two-dimensional SDS-PAGE. Autoradiography showed a spot corresponding to a protein of 55 kD and pI of 5.7- RESULTS: Amino acid sequencing revealed the 55 kD pr carboxylesterase. The biological activity of purified hur carboxylesterase and of an antiserum against carboxyle on sporozoite invasion in vitro was evaluated. Human carboxylesterase as well as a rabbit antiserum against carboxylesterase inhibited the invasion of P. falciparum sporozoites into primary human hepatocytes in culture. number of carboxylesterase cDNA clones were isolated human liver cDNA library. Sequence analysis revealed tv different iso-types. Immunoaffinity purified recombina carboxylesterase was shown also to inhibit the invasion sporozoites into primary human hepatocytes. Immunocytochemical analysis of the localisation of carboxylesterase in primary cultures of human hepatocy using specific antibodies, showed its presence inside th hepatocytes and on the membrane. CONCLUSIONS: Carboxylesterase plays a role in the invasion process of falciparum sporozoites into human hepatocytes in vitro. implications of these findings are further discussed.

PMID: 9365045 [PubMed - indexed for MEDLINE]

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1: Gene 1997 Oct 24;200(1-2):91-8 Related Articl

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Partial nucleotide sequence and organisation of extrachromosomal plastid-like DNA in Plasmod berghei.

Yap MW, Kara UA, ten Heggeler-Bordier B, Ting RC TM.

Molecular Parasitology Laboratory, School of Biological Sciences, Singapore, Singapore.

The murine malaria parasite Plasmodium berghei contair plastid-like extrachromosomal genome. This genome is 3 size and is transcriptionally active as shown by RT-PCR. sequence analysis of the genome reveals 69.9-95.5% hoi to sequences of the 35-kb extrachromosomal circle fou human malaria species Plasmodium falciparum. Homologo sequences include regions of genes for the ssu-rRNA, ls rpo B and clusters of t-RNAs. Sequence variation betwe two Plasmodium species exists in the non-coding intersp regions. A physical map has been constructed for the P. circle, indicating the EcoRI and HindIII restriction site as the arrangement of the rRNA, rpo B and tRNA genes Arrangement of these genes is similar to that found on falciparum 35-kb circle. The P. berghei circular element

distinct from the mitochondrial 6-kb DNA of both the i
and the human Plasmodium species. Preliminary results i
that the circle may be a useful target for drug therapy

PMID: 9373142 [PubMed - indexed for MEDLINE]

1: Acta Trop 1997 Oct 14;68(1):105-14 Related Articl

ELSEVIER SCIENCE FULL-TEXT ARTICLE

Direct PCR amplification and sequence analysis extrachromosomal Plasmodium DNA from dried spots.

Tan TM, Nelson JS, Ng HC, Ting RC, Kara UA.

Institute of Molecular and Cell Biology, National Univer: Singapore, Singapore.

The Plasmodium parasite possesses two extrachromosor genomes; the mitochondrial genetic element and the extrachromosomal plastid-like DNA. The latter has only fully described for one culture strain of P. falciparum. I study, a rapid procedure for amplifying plastid DNA fro blood spots of blood infected with different malaria sp developed. PCR amplification of a 595 bp fragment with plastid-like large subunit ribosomal-RNA (LSU-rRNA) g achieved using primers derived from the P. falciparum s The PCR product was observed in all Plasmodium species examined. Sequence analysis of amplified products hom to an LSU-rRNA fragment of the plastid-like extrachro circle revealed extensive conservation between Plasmoc species including P. falciparum, P. vivax, P. malariae and I

bergner.

PMID: 9352006 [PubMed - indexed for MEDLINE]

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SV   U79731.1
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DE   Plasmodium berghei extrachromosomal plastid PB-1, ORF470 gene, partial cds,
DE   tRNA-Thr, large subunit ribosomal RNA, tRNA-Met, tRNA-Arg, tRNA-Val,
DE   tRNA-Arg, tRNA-Leu, tRNA-Asn, tRNA-Ala, and small subunit ribosomal RNA
DE   genes, complete sequences.
XX
KW   .
XX
OS   Plasmodium berghei
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
XX
RN   [1]
RP   1-5849
RX   MEDLINE; 98038979.
RA   Yap M.W., Kara U.A., ten Heggeler-Bordier B., Ting R.C., Tan T.M.;
RT   "Partial nucleotide sequence and organisation of extrachromosomal
RT   plastid-like DNA in Plasmodium berghei";
RL   Gene 200(1-2):91-98(1997).
XX
RN   [2]
RP   1-5849
RA   Yap M.W.C., Kara U.A.K., Tan T.M.C.;
RT   ;
RL   Submitted (26-NOV-1996) to the EMBL/GenBank/DDBJ databases.
RL   Institute of Molecular and Cell Biology, National University of Singapore,
RL   10 Kent Ridge Crescent S119260, Singapore
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DR   SPTREMBL; O44057; O44057.
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EBI Generic DB Entry Retrieval

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SV   AF182847.1
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DT   25-OCT-1999 (Rel. 61, Created)
DT   25-OCT-1999 (Rel. 61, Last updated, Version 1)
XX
DE   Plasmodium chabaudi from Australia large subunit ribosomal RNA gene,
DE   partial sequence.
XX
KW   .
XX
OS   Plasmodium chabaudi
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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RN   [1]
RP   1-594
RA   Tham J.M., Khoh L.K., Kara A.U.K.;
RT   ;
RL   Submitted (03-SEP-1999) to the EMBL/GenBank/DDBJ databases.
RL   Institute of Molecular and Cell Biology, 30 Medical Drive, Singapore
RL   117609, Singapore
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EBI Generic DB Entry Retrieval

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DT   06-JAN-1999 (Rel. 58, Created)
DT   20-MAR-2001 (Rel. 67, Last updated, Version 3)
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DE   Plasmodium vivax extrachromosomal plastid large subunit ribosomal RNA gene,
DE   partial sequence.
XX
KW   .
XX
OS   Plasmodium vivax (malaria parasite P. vivax)
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
XX
RN   [1]
RP   1-594
RX   MEDLINE; 98013247.
RX   PUBMED; 9352006.
RA   Tan T.M.C., Nelson J.S., Ng H.C., Ting R.C.Y., Kara U.A.K.;
RT   "Direct PCR amplification and sequence analysis of extrachromosomal
RT   Plasmodium DNA from dried blood spots";
RL   Acta Trop. 68(1):105-114(1997).
XX
RN   [2]
RP   1-594
RA   Tan T.M.C., Nelson J.S., Ng H.C., Ting R.C.Y., Kara U.A.K.;
RT   ;
RL   Submitted (15-APR-1997) to the EMBL/GenBank/DDBJ databases.
RL   Institute of Molecular and Cell Biology, National University of Singapore,
RL   10 Kent Ridge Crescent S119260, Singapore
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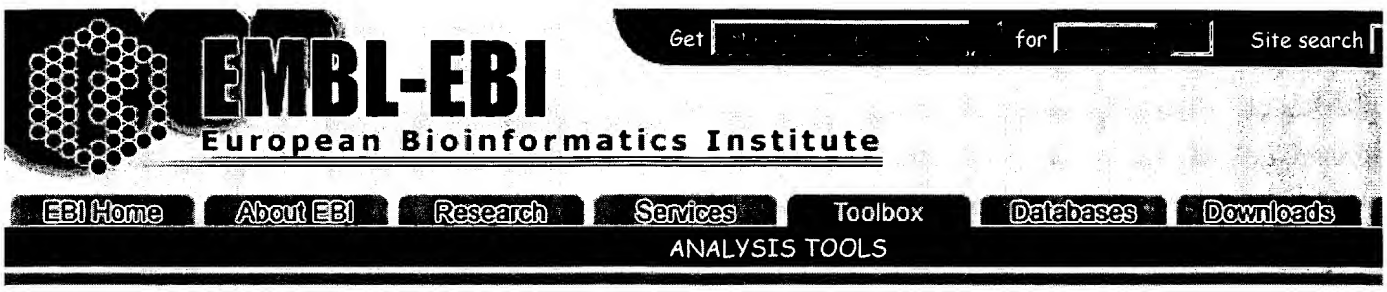

EBI Generic DB Entry Retrieval

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AC   AF182846;
XX
SV   AF182846.1
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DT   25-OCT-1999 (Rel. 61, Created)
DT   25-OCT-1999 (Rel. 61, Last updated, Version 1)
XX
DE   Plasmodium malariae from Burma large subunit ribosomal RNA gene, partial
DE   sequence.
XX
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XX
OS   Plasmodium malariae
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
XX
RN   [1]
RP   1-594
RA   Tham J.M., Khoh L.K., Kara A.U.K.;
RT   ;
RL   Submitted (03-SEP-1999) to the EMBL/GenBank/DDBJ databases.
RL   Institute of Molecular and Cell Biology, 30 Medical Drive, Singapore
RL   117609, Singapore
XX
FH   Key             Location/Qualifiers
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FT   source          1..594
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FT                   /db_xref="taxon:5858"
FT                   /organism="Plasmodium malariae"
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EBI Generic DB Entry Retrieval

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ID   PFTRNA     standard; circular DNA; INV; 5142 BP.
XX
AC   X75545;
XX
SV   X75545.1
XX
DT   01-AUG-1994 (Rel. 40, Created)
DT   01-AUG-1994 (Rel. 40, Last updated, Version 3)
XX
DE   P.falciparum gene for tRNA I,A,N,L,R,V,R,M,T
XX
KW   large ribosomal subunit; small ribosomal subunit RNA; transfer RNA-Ala;
KW   transfer RNA-Arg; transfer RNA-Asn; transfer RNA-Ile; transfer RNA-Leu;
KW   transfer RNA-Thr; transfer RNA-Val; trnA gene; trnI gene; trnL gene;
KW   trnM gene; trnN gene; trnR gene; trnT gene; trnV gene.
XX
OS   Plasmodium falciparum (malaria parasite P. falciparum)
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
XX
RN   [2]
RP   1-5142
RA   Wilson R.J.M.;
RT   ;
RL   Submitted (02-NOV-1993) to the EMBL/GenBank/DDBJ databases.
RL   R.J.M. Wilson, National Institute for MEdical Research, Mill Hill, London
RL   NW7 1AA, UK
XX
RN   [3]
RA   Gardner M., Preiser P., Rangachari K., Moore D., Feagin D.,
RA   Williamson D.H., Wilson R.J.;
RT   "Nine duplicated tRNA genes on the plastid-like DNA of the malaria parasite
RT   Plasmodium falciparum";
RL   Gene 140:307-308(1994).
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EBI Generic DB Entry Retrieval

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AC   X95275;
XX
SV   X95275.1
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DT   29-JAN-1996 (Rel. 46, Created)
DT   14-FEB-1997 (Rel. 50, Last updated, Version 24)
XX
DE   P.falciparum complete gene map of plastid-like DNA (IR-A)
XX
KW   LSU rRNA gene; ORF 101; ORF470; ORF51; rpoB gene; rpoC gene; rpoD gene;
KW   rps2 gene; SSU rRNA gene; tRNA-Ala; tRNA-Arg; tRNA-Asn; tRNA-Ile; tRNA-Leu;
KW   tRNA-Met; tRNA-Val.
XX
OS   Plasmodium falciparum (malaria parasite P. falciparum)
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
XX
RN   [1]
RA   Wilson R.J.M., Denny P.W., Preiser P.R., Rangachari K., Roberts K., Roy A.,
RA   Whyte A., Strath M., Moore D.J., Moore P.W., Williamson D.H.;
RT   "Complete gene map of the plastid-like DNA of the malaria parasite
RT   Plasmodium falciparum";
RL   J. Mol. Biol. 261:155-172(1996).
XX
RN   [2]
RP   1-15421
RA   Wilson R.J.M.;
RT   ;
RL   Submitted (23-JAN-1996) to the EMBL/GenBank/DDBJ databases.
RL   R.J.M. Wilson, National Institute for Medical Research, Mill Hill, London
RL   NW7 1AA, UK
XX
DR   SPTREMBL; Q25799; Q25799.
DR   SPTREMBL; Q25800; Q25800.
DR   SPTREMBL; Q25801; Q25801.
DR   SPTREMBL; Q25802; Q25802.
DR   SPTREMBL; Q25803; Q25803.
DR   SWISS-PROT; P21421; RPOB_PLAFA.
DR   SWISS-PROT; P21422; RPOC_PLAFA.
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CC   Related sequences X52177, X57167, X61660, X74308, X75544, and
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FH   Key             Location/Qualifiers
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EBI Generic DB Entry Retrieval

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AC   X61660;
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SV   X61660.1
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DT   11-SEP-1991 (Rel. 29, Created)
DT   27-SEP-1995 (Rel. 45, Last updated, Version 22)
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DE   Plasmodium falciparum gene for a large subunit ribosomal RNA from the
DE   inverted repeat within the 35-Kb circular DNA
XX
KW   inverted repeat; ribosomal RNA; ribosomal RNA large subunit.
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OS   Plasmodium falciparum (malaria parasite P. falciparum)
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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RN   [1]
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RA   Gardner M.J.;
RT   ;
RL   Submitted (22-AUG-1991) to the EMBL/GenBank/DDBJ databases.
RL   M.J. Gardner, Div of Parasitology, National Inst for Medical Research, The
RL   Ridgeway - Mill Hill, London NW7 1AA, UK
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RN   [2]
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RX   MEDLINE; 93219063.
RA   Gardner M.J., Feagin J.E., Moore D., Rangachari K., Williamson D.H.,
RA   Wilson R.J.M.;
RT   "Sequence and organization of large subunit rRNA genes from the
RT   extrachromosomal 35-Kb circular DNA of the malaria parasite Plasmodium
RT   falciparum";
RL   Nucleic Acids Res. 21:1067-1071(1993).
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WEST Search History

DATE: Tuesday, December 10, 2002

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L1	plastid$.clm. or $plastid.clm.	73	L1
L2	L1 and (malar$ or plasmodi$).clm.	2	L2
L3	L2 and (detect$ or determin$ or measur$ or hybridi$)	2	L3

END OF SEARCH HISTORY

WEST Search History

DATE: Tuesday, December 10, 2002

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L1	berghei	446	L1
L2	L1 same plastid$	0	L2
L3	L1 same ($plastid)	0	L3
L4	L1 and ($plastid or plastid$)	2	L4
L5	($berghei or berghei$)	831	L5
L6	L5 not l1	385	L6
L7	L6 and ($plastid or plastid$)	3	L7
L8	L7 not l4	3	L8

END OF SEARCH HISTORY

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Search Results - Record(s) 1 through 2 of 2 returned.

☐ 1. Document ID: US 6313090 B1

L3: Entry 1 of 2 File: USPT Nov 6, 2001

DOCUMENT-IDENTIFIER: US 6313090 B1
TITLE: Methods for treating parasitic infection using thiopeptides

Detailed Description Text (13):
The thiopeptides of the present invention can be administered to the subject in amounts sufficient to treat the parasitic infection in the subject as desired. Optimal dosages used will vary according to the individual and the particular parasitic infection, on the basis of age, size, weight, condition, etc, as well as the particular treatment effect being induced. One skilled in the art will realize that dosages are best optimized by the practicing physician and methods for determining dosage are described, for example, in Remington's Pharmaceutical Sciences (36).

Detailed Description Text (14):
In a preferred embodiment, the thiopeptide of the present invention can be administered to a human or a non-human animal in a pharmaceutically acceptable carrier in a dosage range of about 50 to 550 mg/kg/day and is preferably administered in a dosage of about 500 mg/kg/day. Treatment can be continued for an indefinite period of time, as indicated by monitoring of the signs, symptoms and clinical parameters associated with the parasitic infection according to protocols standard in the art for monitoring parasitic infections. Examples of the parameters that would be monitored can include, but are not limited to, amount and frequency of diarrheal excretion, oocyst excretion, culture of the parasite in body fluids and tissues, body weight and blood chemistry and urine analysis of hepatobiliary function. Oocyst excretion can be measured by quantitation of acid-fast stained stool specimens, ELISA antigen capture, immunofluorescence assay, DNA amplification, etc., according to protocols well known in the art.

Detailed Description Text (24):
Assay of Growth inhibition. Thiostrepton (1525 u/mg; Calbiochem) and anisomycin (Sigma) were dissolved at 100 mM in DMSO (Pierce). P. falciparum (strain 3D7) (44) was maintained in culture with human erythrocytes (5% hematocrit) in RPMI-1640 (Life Technologies) supplemented with HEPES and sodium bicarbonate and human sera (10%) under standard conditions (18,19). The growth inhibition assay was conducted as described (20). Briefly, the parasitemia was adjusted to 0.1% parasitemia, 2.5% hematocrit and 200 .mu.l aliquots placed in wells of a microtitre dish. Serial dilutions of drugs were made in RPMI. Thiostrepton was diluted to 10 mM in DMSO before the serial dilutions in RPMI. Aliquots (20 .mu.l) were added in triplicate to the cultures in the microtitre plate, mixing well. At the highest concentrations (final 0.2mM), thiostrepton precipitates. After incubation for 48 hours under standard conditions, [2,8-.sup.3 H]-hypoxanthine Moravek Biochemicals, 12.5

Ci/mmol) in RPMI (20 .mu.l, 0.05 mCi/ml) was added to each well. After incubation for a further 24 hours, the cultures were lysed and incorporated radioactivity was measured with an automated counter.

Detailed Description Text (26):
As of organelle and cyloplasmic transcript levels. RNA polymerase transcript levels were assessed by comparing the amounts of RNA synthesized at timepoints following drug treatment. Cultures of P. falciparum (3.2% parasitemia, 5% hematocrit) were treated with thiostrepton at 8 .mu.M and rifampin (Sigma) at 80 .mu.M; near the IC.sub.99 values (this study and ref. 22). Aliquots (5 ml) of treated and control cultures were removed and immediately processed for RNA with a guanidinium thiocyanate solution, according to the manufacturer's directions (RNAgents, Promega). All RNA samples were dissolved in 50 .mu.l DEPC-treated water, DNase I treated as previously described (23) and an aliquot (1 .mu.l) was removed for RT-PCR First strand synthesis of cDNA was completed with a random hexamer (Superscript Preamplification System, Life Technologies). One-tenth of the CDNA product was utilized for PCR of rpoB/C, MSA1, and rRNA. Primers corresponding to the 3' region of rpoB, 5'-GGGCTTTAGAAGCTTTTGG-3' (SEQ ID NO:1), and the 5' region of rpoC, 5'-CCATTTAAAATTGGTAATCCTG-3' (SEQ ID NO:2) were applied as described (2,3) for PCR of nascent rpoB/C transcripts. Reactions were cycled with the following parameters: 94.degree. C./30 seconds, 42.degree. C./30 seconds, 72.degree. C./60 seconds, 35 cycles. Primers for amplification of nucleotide 64 to 614 of MSA1 with 5'-GTGTGATAATATTCATGG-3' (SEQ ID NO:3) and 5'-GGAGAGCATTTGGTG-3' (SEQ ID NO:4)(24) and the small subunit rRNA with oligonucleotides 841 and 844 (23) were used for amplification reactions following the parameters in the respective references except with 35 cycles. Samples were also analyzed after 25 cycles of amplification to ensure detection in the linear range of the amplification reaction, with similar results. Following electrophoresis of aliquots from the amplification reactions on 1% agarose:TBE gels, samples were transferred to nylon membranes (GeneScreen Plus, DuPont) and hybridized as described (25). The amplification products were probed with 5'-.sup.32 P-labeled oligonucleotides. The rpoB/C products were probed with 5'-GTTTAGCTATTAATATAGAAGC-3' (SEQ ID NO:5) (nucleotide 2009-2030 of rpoB) and 5'-CGGAGAGGTATTAATACC-3' (SEQ ED NO:6) (nucleotide 108-125 of rpoC), in 5.times.SSC, 10 mM sodium phosphate, 0.05% sodium pyrophosphate, 1% sodium dodecyl sulfate, 5.times.Denhardt's solution, 100 .mu.g/ml yeast tRNA, 42.degree. C. and washed in the hybridization solution lacking Denhardt's and tRNA at 37.degree. C., three times. The final wash was 1.times.SSC, 0.5% sodium dodecyl sulfate, 42.degree. C. followed by autoradiography. The same results were obtained with either probe. The MSA1 amplification products were similarly probed with 5'-AAACTTGTGTTCGGATATAG-3' (SEQ ID NO:7) and the rRNA products with oligonucleotide 842 (23).

Detailed Description Text (28):
The target of inhibition by thiostrepton. In the absence of a direct measure of plastid-like organelle protein synthesis, assay of mRNA levels by RT/PCR provides a sensitive assay for the selective effect of thiostrepton on the plastid-like organelle. The presence of a protein encoded by the organelle, identified in the 35-kb genome as a homolog of eubacterial RNA polymerase encoded by the rpoB and rpoc genes (5), was assayed during treatment. Selective inhibition of the plastid-like RNA polymerase with rifampin provides a comparison with the effect of thiostrepton, since prokaryotic RNA polymerases are sensitive to rifampin. The synthesis of the rpoB/C mRNA encoded by the 35-kb genome was then compared to a nuclear-encoded mRNA On the basis that the 35-kb encoded rpoB and rpoC are transcribed as a polycistronic mRNA (3), nascent transcripts were assayed at various timepoints during drug treatment by RT/PCR of the mRNA including the intergenic spacer between rpoB/C. Also, the sensitivity of RT/PCR provides a relative estimate of the mRNAs corresponding to those encoded on the 35-kb genome versus those of nuclear-encoded mRNAs. Amplification of part of the mRNA corresponding with Merozoite Surface Antigen (MSA1) was chosen as a nuclear-encoded mRNA, as this is abundant in erythrocytic stages of P. falciparum (24). As a control, a section of nuclear-encoded SSU rRNA was also amplified as this is unaffected by antibiotics.

Detailed Description Text (35):

Intact C. parvum oocyst asset 3.0.times.10.sup.4 C. parvum GCH1 oocysts per well were incubated in the above-mentioned concentrations of drug at 37.degree. C. (8% CO.sub.2) on confluent MDBKF5D2 cell monolayers in 96 well microtiter plates. The level of infection in each well was determined and analyzed by immunofluorescence assay at 48 hours, using C. parvum sporozoite rabbit anti-serum (0.1%) and fluorescein-conjugated goat anti-rabbit antibody (1.0%). Percent inhibition was calculated by subtracting the mean parasite/drug from the mean parasitelmedium, divided by the mean parasite/medium, all of which was multiplied by 100. The analysis was performed using MCID and an inverted microscope.

Detailed Description Text (41):
Intact C. parvum oocyst assay . 3.0.times.10.sup.4 C. parvum GCH1 oocysts per well were incubated in the above-mentioned concentrations of drug at 37.degree. C. (8% CO.sub.2) on confluent MDBKF5D2 cell monolayers in 96 well microtiter plates. For some monolayers, the oocysts were incubated in DMEM on the cell monolayers for four hours, at which time the monolayers were washed and then drug was added to the wells. The level of infection in each well was determined and analyzed by immunofluorescence assay at 48 hours, using C. parvum sporozoite rabbit anti-serum (0.1%) and fluorescein-conjugated goat anti-rabbit antibody (1.0%). Percent inhibition was calculated by subtracting the mean parasite/drug from the mean parasite/medium, divided by the mean parasite/medium, all of which was multiplied by 100. The analysis was performed using MCID and an inverted microscope.

Detailed Description Text (47):
Intact C. parvum oocyst assay. 3.0.times.10.sup.4 C. parvum GCH1 oocysts per well were incubated in the above-mentioned concentrations of drug at 37.degree. C. (8% CO.sub.2) on confluent MDBKF5D2 cell monolayers in 96 well microtiter plates. The level of infection in each well was determined and analyze by immunofluorescence assay at 48 hours, using C. parvum sporozoite rabbit anti-serum (0.1%) and fluorescein-conjugated goat anti-rabbit antibody (1.0%). Percent inhibition was calculated by subtracting the mean parasite/drug from the mean parasite/medium, divided by the mean parasite/medium, all of which was multiplied by 100. The analysis was performed using MCID and an inverted microscope.

Detailed Description Text (51):
SCID mice (Taconic Farms, Germantown, N.Y.), preconditioned with monoclonal antibodies to interferon as described (41), were given an acute infection of C. parvum (10.sup.7 oocysts given orally). A total of five mice in two groups were used. One group received 500 mg/kg/day (in two doses of 250 mg/kg) of thiostrepton six days post-infection and the other group received a placebo. Treatment lasted ten days and oocyst shedding was measured by counting the number of oocysts in 30 fields under high power microscopy of acid-fast stained fecal smears and calculating the mean for each group as described (41). The results in FIG. 1 showed that thiostrepton significantly reduced oocyst shedding (shaded bars) compared to placebo (black bars). These data are summarized in Table 7. Mucosal scores describe the extent of mucosal infection detected in formalin-fixed sections of tissue samples from various gut sites (pyloric region of stomach, liver, gallbladder, mid-small intestine, terminal ileum, cecum and colon) taken during necropsy. Scoring was as follows: 0 (no infection) to 5 (maximal infection) and was expressed as the combined score of the number of gut sites examined.

CLAIMS:

1. A method for treating a parasitic infection in a subject infected with a parasite having a plastid-like organelle, comprising administering to the subject an infection treating amount of a thiopeptide in a pharmaceutically acceptable carrier, wherein the subject is a mammal.

4. The method of claim 3, wherein the parasite is selected from the group consisting of Plasmodium, Toxoplasma and Cryposporidium species.

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7. The method of claim 4, wherein the parasite is Plasmodium.

12. A method for treating Cryptoporidium infection in a subject infected with a parasite having a plastid-like organelle comprising administering to the subject an infection treating amount of a thiopeptide in a pharmaceutically acceptable carrier, wherein the subject is a mammal.

17. A method for treating a parasitic infection in a subject infected with a parasite having a plastid-like organelle, comprising administering to the subject an infection treating amount of a thiopeptide in a pharmaceutically acceptable carrier, wherein the parasitic infection is caused by a member of the Microspora phylum or Ascetospora phylum.

21. A method for treating a subject infected with a parasite comprising administering a thiopeptide to the subject, wherein the parasite is selected from the group consisting of Plasmodium, Toxoplasma, and Cryptospordium.

22. The method of claim 21 wherein the parasite is Plasmodium.

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L3: Entry 2 of 2 File: USPT Jul 31, 2001

DOCUMENT-IDENTIFIER: US 6268160 B1
TITLE: Method of screening for anti-malarial compounds

Brief Summary Text (12):
(ii) determining whether the compound binds to or inhibits the protein, any such binding or inhibition being indicative that the compound is an anti-malarial.

Brief Summary Text (15):
(ii) determining whether the compound binds to said RNA or said fragment, any such binding being indicative that the compound is an anti-malarial.

Drawing Description Text (5):
FIG. 3A shows a Southern blot of endonuclease-restricted malarial genomic DNA hybridised with a PftufA-specific PCR product as probe. A single band for the 35 kb plastid was obtained for each restriction digest.

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Drawing Description Text (6):
FIG. 3B shows cross-hybridisation between endonuclease-restricted malarial genomic DNA and the yeast tufM gene, indicating the possible presence of a malarial version of tufM.

Drawing Description Text (13):
FIG. 11 shows slot blots of RNA fractioned on sucrose gradients. Pretreatment with anisomycin blocked the puromycin-induced shift of the hybridization signal for P.falciparum cytosolic 23S ribosomes but not the plastid 16S ribosomes. A-C. Blots hybridized with a probe for the cytosolic large subunit (23S) rRNA. Anisomycin blocked the puromycin-induced shift. D-F. The same blots hybridized with a probe for the plastid-encoded small subunit (16S) rRNA. Anisomycin did not block the puromycin-induced shift.

Drawing Description Text (14):
FIG. 12 is a slot blot showing the puromycin-induced shift of the hybridization signal for plastid mRNA specifying EF-Tu.

Drawing Description Text (15):
FIG. 13 contains immunoblots showing that binding of antibiotics modifies migration of EF-Tu.GDP in native polyacrylamide gels. Two segments of the same gel show A) heterologously expressed Pf EF-Tu.sub.pl protein detected with a malaria peptide-specific antibody and B) E.coli EF-Tu detected with a specific antibody (Breidenbach et al 1990). Lanes without antibiotics (1 and 5), lanes with 100 .mu.M antibiotic: GE2270A (2 and 6), enacyloxin IIa (3 and 7), kirromycin (4 and 8). Arrows indicate uncomplexed EF-Tu.

Detailed Description Text (25):
The invention includes an antibody specific for the EF-Tu protein of the invention. The antibody is preferably monoclonal, but may also be polyclonal. The antibody may be labelled. Examples of suitable antibody labels include radiolabels, biotin (which may be detected by avidin or streptavidin conjugated to peroxidase), alkaline phosphatase and fluorescent labels (e.g. fluorescein and rhodamine). The term "antibody" is used herein to include both complete antibody molecules and fragments thereof. Preferred fragments contain at least one antigen binding site, such as Fab and F(ab').sub.2 fragments. Humanised antibodies and fragments thereof are also included within the term "antibody".

Detailed Description Text (31):
Various different assay systems may be used to carry out the screening, but all the assays have in common that the EF-Tu protein of the invention is contacted with test compounds and the ability of each test compound to bind to or inhibit the protein is determined. Any such binding or inhibition is indicative that the compound could be useful as an anti-malarial drug.

Detailed Description Text (32):
The screening assays will generally require one or more controls. It will generally be desirable to include a positive control in the form of a compound known to bind to or inhibit the EF-Tu protein, so as to ensure that the assay system is responding properly. Examples of suitable positive controls include kirromycin (mocimycin) and aurodox (1-methylmocimycin), which we have shown through our experiments to be effective anti-malarials and which are known to inhibit prokaryotic EF-Tu. It will also gcnerally be desirable to include a negative control in the form of a sample containing no test compound, so as to obtain a measurement of the background signal in the assay. If a test compound gives a signal in the assay above that of the background, this is indicative that the compound has given a positive result and could be an anti-malarial.

Detailed Description Text (33):
One convenient type of assay system is a "band shift" system. This involves determining whether a test comopund advances or retards the EF-Tu protein of the invention on gel electrophoresis relative to the EF-Tu

protein in the absence of test compound. The mobility of GDP complexed EF-Tu is decreased with GE2270A but increased with enacyloxin IIa or kirromycin.

Detailed Description Text (36):
(ii) determining the amount of the labelled reference compound that is bound to the protein; and

Detailed Description Text (37):
(iii) comparing the amount of bound labelled reference compound determined in step (ii) with the amount of said compound that binds to the protein in the absence of the test compound;

Detailed Description Text (39):
The amount of the labelled reference compound bound to the protein may be measured directly or indirectly. A direct measurement may be carried out by removing assay mixture containing the unbound labelled reference compound and measuring the amount of label that is in the protein fraction. Alternatively, the amount of labelled reference compound bound to the protein could be determined indirectly by measuring the amount of label remaining in the assay solution after removal of the protein fraction, which will be inversely related to the amount that has bound to the protein.

Detailed Description Text (40):
In a competitive binding assay system, the EF-Tu protein may be immobilised on a solid support or may be in solution. The use of immobilised protein has the advantage that, after the binding reaction is complete, the protein/labelled reference compound complex may be separated from the labelled reference compound that remains in solution by simply removing the solution away from the solid support. If, on the other hand, the protein is not immobilised during the assay but rather is in solution, then it will generally be necessary to devise a means for separating the protein/labelled reference compound complex from the uncomplexed reference compound before measuring the amount of label. Such separation could be achieved, for example, by precipitating the protein using an antibody to the protein or by using a non-specific protein precipitation technique.

Detailed Description Text (52):
This information allows the design of assays for screening for further anti-malarial compounds whose mechanism of action operates through the 23S rRNA. These assays involve contacting each of the test compounds with the 23S rRNA or a fragment thereof containing the GTPase binding domain, and measuring any binding of the test compounds to the rRNA or fragment. Any such binding is of course indicative that the compound could be an anti-malarial.

Detailed Description Text (53):
We have already developed one assay for detecting binding to the 23S rRNA. We made a short transcript from DNA encoding the 23S rRNA of the malaria plastid corresponding to the GTPase domain (about nucleotide 1051 to about nucleotide 1108) and found that the transcript bound thiostrepton strongly.

Detailed Description Text (55):
A screening assay for further anti-malarial compounds can be based on a competitive binding assay in which the ability of each test compound to compete with thiostrepton for binding to the Pf 23S rRNA.sub.pl is measured. Such an assay comprises

Detailed Description Text (57):
(ii) determining the amount of thiostrepton (or other reference compound) that is bound to the rRNA or the fragment; and

Detailed Description Text (60):
In a screening assay based on the invention for further anti-malaria compounds, it would be necessary to use appropriate controls. A good positive control would be to use a compound known to compete with thiostrepton (or with the other reference compound) to ensure that the assay is working properly; a positive result for the known competitor in the assay would indicate that the assay had worked correctly. It would also generally be desirable to use a negative control comprising, for example, a sample in which no thiostrepton or test compound is present; this would enable the background signal in the assay to be determined and any signal above the background would indicate binding to the 23S rRNA.

Detailed Description Text (66):
In an experiment with RNase (Cox 1969), total polysomes were incubated with a range of concentrations of RNase (1-13 ng ml.sup.-1 ribosomes, Boehringer) prior to centrifugation for 30 min at 26.degree. C. In other experiments, polysomes were dissociated to monosomes and subunits by the incorporation of puromycin; here the total ribosome preparation was incubated for 20 min at 37.degree. C. with 2 mM puromycin in the "high salt" buffer to which was added 2 mM GTP, 10 .mu.lml.sup.-1 RNAsin (39 U.mu.l.sup.-1, Promega) and 1 mM DTT. In some experiments, ribosomes were incubated with both anisomycin (Sigma) and puromycin. Anisomycin was added at 3 mM for 10 min at 37.degree. C. followed by incubation with puromycin as above (Cundliffe et al 1974). After ribosome fractionation on the sucrose gradients, RNA was extracted with phenol/chloroform/isoamyl alcohol (Chomczynski it al 1987), precipitated in ethanol and blotted on to nylon membranes (Gene Screen, Trade Name) using a slot-blot apparatus (Scot-Labs). Hybridization was carried out with .sup.32 P-labelled DNA prepared from either cloned fragments of the 35 kb plDNA of P.falciparum, PCR products amplified from it, oligonucleotides based on its sequence (Wilson et al 1996), or with PCR products based on the sequence of Pf 28S cytosolic rRNA (McCutchen et al 1988). Hybridization signals were quantitated using a Molecular Dynamics phosphor imager.

Detailed Description Text (68):
EF-Tu model--Pf EF Tu.sub.pl was modelled by homology with the known 3D structures determined by X-ray crystallography of EF-Tu.GTP (Berchtold et al 1993) and EF-Tu.GDP (Polekhina et al 1996) both from Thermus aquaticus. Modelling was carried out with the WHAT-IF program package (Trade Name, Vriend 1990), as described in Tews et al 1996. Alignments had to be adjusted manually because of small gaps and insertions. An iterative procedure of the automated model-building algorithm checked and corrected the alignments until no errors were detectable. Three insertions in the Pf EF-Tu.sub.pl sequence had to be deleted: Leu 190, Pro263 and Leu359-Val363. The final alignment with the T. aquaticus structure had single residue gaps in the Pf sequence between Leu41 and Ser42 as well as residues Asn209 and Ile2 10. Co-ordinates for the C (alpha) backbone were copied from the known structure for overlapping segments and the atoms for the amino acids Gly, Ala and Pro were placed directly in their calculated positions. All remaining residues were assigned to Ala before the order in which side changes had to be placed was calculated by the algorithm implemented by the program. Atoms were subsequently placed using a position-dependent amino acid rotamer library. The model was refined geometrically and re-numbered according to the P.falciparum sequence.

Detailed Description Text (69):
Heterologous expression--The malarial plastid tufA gene was amplified by PCR, cloned into the TA vector (Trade Name, Invitrogen) and its sequence determined (Wilson et al 1996). Re-cloning into the expression vector pGEX (Trade Name, Pharmacia) was carried out with a PCR product generated using 5' and 3' primers providing custom-made restriction sites. Transfectants in E.coli (strains DH5 alpha, Sure, JM109) were found mostly to carry deletions within the tufA sequence, but one clone in JM109 contained the complete insert (sequenced on a single strand). This was expressed as a fusion protein of the expected size by induction of mid-log phase cultures with 50 .mu.M isopropyl-.beta.-D-thiogalactoside (IPTG) at 37.degree. C. or 27.degree. C. The insoluble fusion protein was solubilized in 5M guanidinium HCl and refolded by dilution (Lin et al 1991).

Detailed Description Text (74):
Ribosomes from erythrocytic parasites were fractionated by centrifugation on linear gradients (20-50% sucrose) and RNA was extracted from fractions collected over the length of the gradients. Slot blots of the RNA were hybridized with .sup.32 P-labelled DNA probes prepared from either cloned fragments of Pf plDNA, PCR products based on its sequence, or kinased oligonuceotides. As shown in FIG. 11 C&F, hybridization with probes for the large.sub.(cytosolic) or small.sub.(plastid) subunit rRNAs gave signals extending to the bottom of the gradient, indicative of rRNA incorporated in polysomes. Supportive evidence was obtained by limited digestion of the total ribosome preparation with RNase (13 ng RNase/mg ribosomes for 30 min at 26.degree. C.) before fractionation--this causes dissociation of the polysomes (Cox 1969) and shifted the hybridization signal up the gradient (data not shown). More specific evidence for a subset of polysomes belonging to the plastid compartment was obtained by incubating total ribosomes with 2 mM puromycin in the presence of GTP, 0.3M KCl and 1 mM DDT prior to density gradient fractionation: puromycin acts as an analogue of the 3' terminal adenosine of aminoacylated tRNAs and is incorporated into nascent peptide chains, terminating translation and dissociating polysomes (Gale et al 1981). Incubation with puromycin caused a shift of both the cytosolic and plastid rRNA hybridization signals up the gradient (FIG. 11, B&E). The specificity of the puromycin-shift was confirmed by pre-treating Pf ribosomes with the antibiotic anisomycin which binds only to eukaryotic ribosomes and prevents puromycin incorporation (Gale et al 1981). As shown in FIG. 11A, anisomycin blocked the puromycin-induced shift of the hybridization signal for Pf 28S cytosolic rRNA, whereas hybridization of the same blot with a probe for Pf 16S rRNA.sub.pl showed the puromycin-shift of the plastid subset of polysomes was not blocked (FIG. 11D).

Detailed Description Text (75):
Similar results were obtained with a probe for an mRNA specified by the plDNA. FIG. 12 shows the puromycin-induced shift of the hybridization signal for mRNA specifying EF-Tu.sub.pl.

Detailed Description Text (76):
To quantitate the relative proportions of the hybridization signals generated by different species of RNA, slot blots were hybridized with .sup.32 P-labelled oligonucleotides, known amounts of DNA being used as appropriate standards. The 28S cytosolic rRNA was estimated to be 80-fold more plentiful than 16S rRNApl and 2000-fold more plentiful than the mRNA specifying EF-Tu.sub.pl (data not shown). These results and the puromycin-shifts are consistent with the presence of actively translating plastid ribosomes in blood cultures of malaria parasites.

Detailed Description Text (81):
When hybridized with a PftufA-specific PCR product under stringent conditions, Southern blots of endonuclease-restricted malarial genomic DNA gave a single band of the size predicted (FIG. 3A). At low stringency no other bands were revealed that might have corresponded to the nucleus-encoded mitochondrial gene tufM (Nagata et al, 1983; Wells et al. 1994). The likely presence of a malarial equivalent was indicated, however, by cross-hydridization at low stringency with a PCR product based on the yeast tufM gene (FIG. 3B).

Detailed Description Text (99):
The material tufA gene in pGEX was expressed as an insoluble fusion protein in E.coli JM 109. The protein was detected either with antibodies to the GST tag or with antibodies to a specific peptide sequence in domain I (IQKNKDYELIKSN SEQ ID NO:7) not found on E.coli EF-Tu. Washed inclusion bodies were dissolved and refolded by dilution (Lin et al 1991). This yielded a small amount of refolded protein that migrated in native acrylamide gels as a spontaneously cleaved product and we used this to show that the expressed protein forms complexes with kirromycin and other drugs that bind to different sites on EF-Tu. As shown in FIG. 13, the mobility (M.sub.r) of the expressed malarial protein was advanced or retarded in these complexes in the same characteristic way described for E.coli EF-Tu (Cetin et al 1996): the M.sub.r of the GDP form of the complex decreased with GE2270A, but increased with enacyloxin IIa or kirromycin. These results show that the

heterologously expressed Pf EF-Tu.sub.pl can adopt a native conformation and bind the classical antibiotic inhibitors.

CLAIMS:

1. A method for screening a compound for anti-malarial activity with malarial elongation factor-Tu(EF-Tu) protein, which method comprises

(i) contacting the compound with the EF-Tu protein encoded on the 35 kb circular plastid DNA of Plasmodium falciparum; and

(ii) determining whether the compound binds to and inhibits the protein, any such binding and inhibition suggesting that the compound may have anti-malarial activity.

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